

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCACCA**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTCCAAAGGCTCCCTGTTGTGAAGAATTCATCAGCAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAAATTTGGGATCCGGCGTGGGA
 GAAC TGGCCAAGAAGCTCAAAGAGGCAGCATTGGAAACCATCGATTGGAATAATATTTAAATTT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGCTGCTGTTGGTCTTGGAGCATTTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCGAGGCCAAAGCATCTTGCTTGGTTGCTACATTTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCCACTGTGGCCATGTGTGCGCCCAAGTGAAGAATTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGGCACTCTTTACTCAGTGGCAATGTACGGTGGAT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAATAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTGTTTAAATGGGGCAGATATGC
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCTATCATA
 TTTAAATGTTCCGGTAATGTGATGCCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAAATAAGCACACACATTTTCAATTTCTCATGTTTGAAGTATTTTAAATGTT
 TTGGTGAATGTGAAGCTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTTGTACATTCATTT
 GCTGAACCTTAACAAACTGTTTATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTTCATGTTTGAATTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATATTTCTCAAGAGAAAATATTCAAAGCATGAAATATGTGCTTTTCCAG
 AATACAAACAGTATACTCATG

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGA

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRGTGQEL
KEAALEPSMEKIFKIDQMGRWVFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTFVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290
300
310
320
330

AAGGCTGCGCTCGCTCTCGGAAATTCGGTGGCGCAGCTCGCGCGCTCTCGCCCTTCGATC
 CGCGGCTTCGGCGGCTTCCACATGACAGCATTAACAGTGGCGAGCGCGCGCTGTGAGGG
 CGCTCGGCACGGGAGAGCTCGGGCGGCTTCGTGCATCTTGGCATCTTGGTCTGGGTGCGAAATCGCTCGG
 ACATCGAGGACATGGTTCAGGAGCATCCCGGCGAICACGGCGCTATTTGTTGCGCGGCACGCTG
 GCGCTGCCCTTGGTCGGCAAACTCGGCCCTCATCGCCGCGGCTACCTCTCTCTCGGCCGCA
 AGCCTTCCTTTATTCGTTTCAGATTTGGAGGCGCAATCATGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAATCGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTTACGACGA
 CTTGAAGAACAGGAGCTTTTATGGGAGGCCACGACATATTATTCATGCTCCTCTTTAACTGT
 GATTTGCATCTGTCGATTACTGGCTTAGCAATGGATATGCAGTTCGCTGATGATTCCTCTGATC
 TGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGTTGTATCATTTTGGTTTGGAA
 ACAGGATTTAAAGCCGCTGTAATTAACCTGGGTATPCTTGGATTCAACTATATCATCTCGGAG
 TCTCGTAATCAATGAGCTATTGGAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCCCAATGGACTTGGGAGGAGAAATATTTCTATCCACACCTCAGTTTGTTCAGCCGTGG
 CTGCCCACTAGGAGAGGAGGATCATCAGGATTTGGTGTGCCCTGTAGCATGAGGCGAGC
 TGTCTCATCAGAATGGCGGAGGCGGGAAGACAACACTGGGGCGAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGGGCGGCTCGGGACGCGGCTCTCTCAAGCCACATTTCTCCAGTGCTGGGTGT
 CACTTAAACAACTCGGCTTCGGCTAAACATCTTGGACGTCACCCACATGAATGTAGTCTTTC
 AGTAGCAAGCAAAAGTTCTTAAATCCCGAAGAAAATATAAGTGTCCACAGTTTTCAGAT
 TCTCATTTCAAGTCTCTACTGCTGTGAAGAACAATAACCAACTGTGCAAAATGCAAAATCGAC
 TACATATTTTGGTGTCCTCTCTCTCCCTTCCTGGCTGAATAATGGGTTTAGGGGGTCTCT
 AATCTGCTGGCATTTGAGCTGGGGCTGGGTACCAAAACCTCTCCAAAAGGACCTTATCTGT
 TCTTGACACATGCTCTCTCCACITTTTCCCAACCCCACTTTGCAACTAGAAAAGTTGT
 CCAATAAAATTGCTCTGCCCTTGACAGGTTTCGTGTTATTTAGCTTTTCCCAAGCTGGTCT
 ACCAACATCATTTTCAGCTATTTTCCCTTTTGGTGGCAGAACCTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCGGTTGTT
 AACCGTTTGGCCATCTTCAGATATTTTATAAAAAAGTACCACTGAGTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACAGGAGGTTGGTGCTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTGATGGAAGTGCAGTAACTAGGTTAGGTTTAAACATGGGGGATGCACCC
 TTTGGGTTTCATATGATGCCCTACTGGCTTGTGTGAGCTGGAGTAGTGGGTGTGCTTTGTGT
 TAGGAGATTCCGATATGTTGGCTACAGGAGGATGCTCTCTTTGAGAGGTTCTGGGCACTG
 ATTTCCCAATTCATCTCATCTGGATATGTTCTCATTTGAGTAAGAGGAGGAGACCCCTATA
 CGCTATTTAAATGTCACTTTTTTGCTATGCTCCCGGTTTTTGGTCATGTTCAATTAAATGT
 GAGGAGGCGCGAGCTCTCTCTCGACGCTAGATCTTTTTTAAAGCTAATGTGAAGACATCT
 AGGGAATAACATGATTTAAGGTTGAAGTGCTTTAGAACTATTTGGGTGTGGAGGTGTGTTA
 TTTGAGTCAATGAATGTACAAGCTCTGTGAATCAGACCGAGCTTAAATCCCAACCTTTTT
 TCGTAGGTGGGCTTTTCCATTCAGAGCTTGGCTCATAAACAAAATAAGTTTITGAGGGCA
 TGGCTTTCTCACACGATTTATTTATTTATGACGTTATCTGAAGACGAGCTGTGAGGACGAT
 ATTTGAGTGGCTGTACACATCTGAGGCAATTAAGAGGTTTGGTGTGATGATGATGATGAT
 TCTCAGGAATATCTGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 TATTTCTCATATTTAATTTATATGATAAAATAGGTGGGAGGCTGCAACTACTGTGCTG
 TGTATTTGTGTTTCATCTGTGCCACATAAAGTTTACTGTAAATTTTAGAGGCATTA
 CCAATTATGTGACAGCTACATCTGTACAGGCTGGAGACTCATTTGATTAAGAATA
 TTTCTGACAGTGAGTGCACCGGAGCTCTGGTGTACCCCTTTACAGTCAAGTGGCTCGGAG
 CAGTCATCTTTTCTCAAAGGTTTACAAGTATTTAGAAGTTTCAGTTCAGGCGCAAAATGTT
 ATGAAGTTATTTCTTTAAACATGGTTAGGAGAGCTGATGACGTTATGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTGTACTTGACAGGCAAAACA
 TGACAGTGGAATCTCTTTTAAAGTGAAGAAAAAATCCTTATTTGTATAAGGACTCCC
 TTTTGTGTAACCAATCTCTTTTATTGGTGTAAAAATGTAATTTAAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCAATTTGCATTAACTGGTTG
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCTAACCGGGGTCGGCGGTCTGGCCTAGGGATCTTCCCCTTGGC
CCTTTGGGGCGGG**CATG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCTCGGAGGCCAGACTGGTCCATCCCCTCTTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
ACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTCCCAAGGGGATGGTGAACATTTTGCAACCCACCCTCAGAAGTTAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAACTTCTCCCTCC
CACAAAAGGCCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
TTATCAGTACTTGAACAGAGAAGCTTCGGCAACGAGAACATATCTCAAGCAGAAGAGAGA
TAAGTTGATGTCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATTGGCAGAGAAAG
GAAAACCCACTGGGAGGTTAGAGGAATGACAGAGAAACCGAAATGACAGCAGAGGAGAAG
CAAACTACTTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAGAGTTATTAATAAG**TA**
ATATTAAGAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLA AEDFTIFKAMMVQKN IEMQLQAIRIIQERNGLVPDCLTDGSDVVS DLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPENTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGGAAAAACAGTCTGTAGTCATCCTGTAAATAGCTCCTTTGCAACAATGTATAC
 ATTCTCGCTAGGTGCCATATTCATTCGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACCTACTGTGAATGTGTCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAAGTAG
 AAATTTGAAATATGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTCGCT
 TTCTTTATTTCTGGATAACTTGATTGCTTCTATGTCTGTCCCTATCTTCAACAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGCTGAA
 GAGGCGCTAAACTGGATCCAGTGGGCTTCCTCTCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCTCGCTTCTTTTCAGAAGTGAGTGTCCAGAAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCTAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGAGGGGAACACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACCTCATTTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTCAGAGGA
 GTAACCGTGATCAGATTAAGAACGTGGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAACGTGATTCCAGGGCCCTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTCTTGATGGCCAGGTTACCACTGTCATTATCACAGAGTGCTGTGCTGG
 TCTTTGACTTCAGGCCCTCCTCGGAATTTTTCTTGAAGCCCATCAGTCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAAGACTAGAAAGACTTA
 CCAAACCCAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTGAACCTTATTTTACATTTTCAGTGTGTTGTAATATTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTGTAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTAGTTACATGCCAAAGT
 CTTCCTCTTTTAAACATTATAAAAGCTAGGTTGTCTCTGTAATTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGCGGATGATGTAGTCTGTGCTAAATTTTTGCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTAGAAATTCATGGGAAATGGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTGGTTCCTAGTCCCATAGTTTACCCTTGATTTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAAATTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGATCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACTTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGATGATATTAATATCTCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACTTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTCTGAT
 GTATTTTGATGTCAGCCAGTTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACCTGTAATATAGAGCTTTTGTGTT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACATTATATAAATTCATTTGTGATATCCACAATAATATGACTGGCAGAAGTTG
 GTGGAATTTGTAATTAATAATTTATTAACCTT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAIPIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHDDAFF
 SPSNSCLLFRSECPKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFVSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCAATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTTATAACAACAGCTCTTCTATTAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGACAGGAGCAT
 CCCGTCTACAGGTCCTCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGCTGCTACCCACAGCATCTCCAAAGCACGTAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCTTCAGATCTAC
 CTATTGG**ATG**TGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGTGCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCGCTCATTGCTACTTCTCTC
 ATCTGGTTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGACAATCGTGGGCCAAGCAGACACGCCTTGTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGGCGGAGCAGAGAACCCCTATGAAGCCACGACGCTG
 AGCCAATGCCTACTTCCGGGGCCTACGGCTGGTCTATGAGCCACGGCCCATACATCAAACCTT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTACCAGTTTGGCTCTGGAGTGTC
 ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAAGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCATTGATGAGGAGAGGCGGCGGAGAAAGAA
 GGCCTGCGAGGCACTGAGGGACGAGGCCAGCAGCTTGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCT**TAG**GGCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGCTTGTCTGAGCAGCTGGACTGCAGTGTCTAGGAAGGGAA
 CTGAAGACTCAGGAGGTGGCCCGAGGACACTTGCTGTCTCAGTGTGGGGCCGGCTGCTCTG
 TGGCTCTCTGCTCCCTCTGCTGCTGCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTATTTTCATAAAAGCTGGAAGC

MWLRWALS L P S S C L W A E P G M P S Q T P W W A S A S A N P P G P A W A L C P G S S S P R P W S L P T S S S G
S C P T S H T A R P I G T C F S I A S L K Q W S R V S M F P T R L S P C S S A T E Q T E R D S A T A Y R M T V E V L G T V L
G T A I G Q G I V G Q A D T P C F Q D F N S S T V S A S Q S A N H T H G T T S H R E T Q K A Y L L A A G V I V C I Y I I C A V
I L I L G V R E Q R E P Y E A Q Q S E P I A Y F R G L R L V M S H G P Y I K L I T G F L F T S L A F M L V E G N F V L F C T
Y T L G F R N E F Q N L L L A I M L S A T L T I P I Q W F L T R F G K K T A V Y V G I S S A V P F L I L V A L M E S N L I
I T Y A V A V A A G I S V A A F L P W S M L P D V I D D F H L K Q P H F H G T E P I F F S F Y V F T K F A S G V S L G
I S T S L D F A G Y Q T R G S Q P E R V K F T L N M L V T M A P I V L I L G L L L F K M Y P I D E R R R Q N K K A L
Q A L R D E A S S S G C S E T D S T E L A S I L

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGTGCAGGT
 ATGAGCAGGCTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTACTGAGTTGTTTAGG
 ACTTTCATTTGTGGCAAACCTTCAGAAAAACAACCTTTTTTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCCTACCAAATG
 CAGCCCAAATCCATGGCAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIIFSYYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGQVFWIRLLLVICGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFOKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGGCNCGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCTGTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTGTGAA
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 17

CCCACGCGTCCGCCCCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGCTGCAC
 CTTGCGCTTGTA¹CTTGCTGTCGACGCGACTGCCCCGCGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTTCCTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCATTGTTTTTGATTGCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTACGCGCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNLVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAA
 TAGAAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGTCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCTAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCACTGGCTGTGCCCGAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTCT
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTCCCATTTCCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCTGTCTTCTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCGCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTDGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELPV
FTHLPFPKDALNKCSSLHPEPVVGSKMHKMPDLFTIGSGEAMLQLIPPFQCRRHQCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

21/330

姓名	性别	年龄	职业	住址	电话
王德胜	男	45	教师	XX路XX号	12345678
李小红	女	32	医生	XX街XX号	98765432
张小明	男	28	工程师	XX巷XX号	56789012
赵大伟	男	50	农民	XX村XX组	34567890
陈丽娟	女	38	护士	XX路XX号	23456789
孙国强	男	42	商人	XX街XX号	10987654
周小芳	女	25	学生	XX路XX号	87654321
吴大刚	男	55	工人	XX巷XX号	65432109
郑小华	女	30	记者	XX街XX号	43210987
冯大伟	男	48	律师	XX路XX号	32109876
马小娟	女	22	歌手	XX巷XX号	21098765
朱大刚	男	52	画家	XX街XX号	10987654
徐小芳	女	27	程序员	XX路XX号	98765432
黄大伟	男	40	科学家	XX巷XX号	87654321
吕小娟	女	35	作家	XX街XX号	76543210
周大刚	男	43	企业家	XX路XX号	65432109
吴小芳	女	29	设计师	XX巷XX号	54321098
郑大伟	男	51	教授	XX街XX号	43210987
马小娟	女	24	模特	XX路XX号	32109876
朱大刚	男	47	厨师	XX巷XX号	21098765
徐小芳	女	31	舞蹈家	XX街XX号	10987654
黄大伟	男	44	音乐家	XX路XX号	98765432
吕小娟	女	26	演员	XX巷XX号	87654321
周大刚	男	49	导演	XX街XX号	76543210
吴小芳	女	33	制片人	XX路XX号	65432109
郑大伟	男	53	制片人	XX巷XX号	54321098
马小娟	女	23	制片人	XX街XX号	43210987
朱大刚	男	46	制片人	XX路XX号	32109876
徐小芳	女	34	制片人	XX巷XX号	21098765
黄大伟	男	41	制片人	XX街XX号	10987654
吕小娟	女	21	制片人	XX路XX号	98765432
周大刚	男	54	制片人	XX巷XX号	87654321
吴小芳	女	36	制片人	XX街XX号	76543210
郑大伟	男	45	制片人	XX路XX号	65432109
马小娟	女	20	制片人	XX巷XX号	54321098
朱大刚	男	43	制片人	XX街XX号	43210987
徐小芳	女	37	制片人	XX路XX号	32109876
黄大伟	男	40	制片人	XX巷XX号	21098765
吕小娟	女	28	制片人	XX街XX号	10987654
周大刚	男	56	制片人	XX路XX号	98765432
吴小芳	女	39	制片人	XX巷XX号	87654321
郑大伟	男	48	制片人	XX街XX号	76543210
马小娟	女	25	制片人	XX路XX号	65432109
朱大刚	男	42	制片人	XX巷XX号	54321098
徐小芳	女	30	制片人	XX街XX号	43210987
黄大伟	男	44	制片人	XX路XX号	32109876
吕小娟	女	27	制片人	XX巷XX号	21098765
周大刚	男	50	制片人	XX街XX号	10987654
吴小芳	女	32	制片人	XX路XX号	98765432
郑大伟	男	46	制片人	XX巷XX号	87654321
马小娟	女	24	制片人	XX街XX号	76543210
朱大刚	男	47	制片人	XX路XX号	65432109
徐小芳	女	31	制片人	XX巷XX号	54321098
黄大伟	男	41	制片人	XX街XX号	43210987
吕小娟	女	21	制片人	XX路XX号	32109876
周大刚	男	54	制片人	XX巷XX号	21098765
吴小芳	女	36	制片人	XX街XX号	10987654
郑大伟	男	45	制片人	XX路XX号	98765432
马小娟	女	20	制片人	XX巷XX号	87654321
朱大刚	男	43	制片人	XX街XX号	76543210
徐小芳	女	37	制片人	XX路XX号	65432109
黄大伟	男	40	制片人	XX巷XX号	54321098
吕小娟	女	28	制片人	XX街XX号	43210987
周大刚	男	56	制片人	XX路XX号	32109876
吴小芳	女	39	制片人	XX巷XX号	21098765

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALET
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLELVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQFGPIPPHTQV
 RNQVYSWLLRLRPSPQGYLSSRPQEMLRASGLTQKWWQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPDLDSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSDRQFHSAVAWQARLESADVKELIP
 EFFFYFPDFLENQNGFDLGLCLQLTNEKVGDVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL
 SQLSCHLDVVVTCLALDTCGIYLSISRDTTCMVWRLHLQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDDGTVIHTVRRQGFAALRPLGATFPGPFIHIALGSEGQIVVQSSA
 WERPGAQVYTSYLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCAT
CCAAAGGCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATATGGGGTCTCTGGGGCTCTTC
TGGACCCTTAAGTGGGTACTGGCCCTGGGGCCAATGCGTCTCGTGGAGCCCTTGGCTCCTT
CTACTGGGGCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
ATAGCCCGGGTCACTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAATAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTCTCTCAGCCAAA
AATGCGTTACTGCTACTCATGCGAAACATTGTGAGGTGGTGCCTGCGACAAAGTGCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGCGTGGGGGTCCGTGCTCTCTTTT
TTTTCTCCGGTCGCATCCCGGGGTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGACCTTCTAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCGGGCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGGCATCAACCTCACTTCGGCTTACAGGTCTCCATTGTGTTT
AAAAAAGAGTTTTAGGCCAGGCGCGCTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAAATGGCTTGAACCCGGGAGGCAGAGGTTGCACTGAGCCGAGA
TCGGCCCACTGCACTCCAACCTGGGTGACAGCACTGTCTCCAAAACAAAACAAACAAA
AAGATTTTTATTAAGATATTTTGTTAAGTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

[illegible]

Figure 1

27/330

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGSEFSEKRTRELEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFPLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

0000722-111902

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTATTTTCTAGTGAAC
 CACGAAGGGACGATACCGAAAAACCCCTCAACCCCAAGGAAATAGACTACAGCCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAGAAAGGACGAAAGAGACAGTATTTTGGAAAGCTAA
 GCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTACAGCTTTTAAACAATT
 GAGTAAAGTACGGTCCGGTCACCA**TG**TGTGACAGCCGCCCTGGGTCCTGGGACGGCTG
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGTGTGGGC
 CAGGGCTCCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCATGTATCTCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCCTGAGATCAGACCCCTACATTAATATACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCGTGCCAGAAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GCGGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCAGCCGGCCAGTTTGTCTGCCCTGCCCTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGAGCTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCTATC
 CTGTACGGCAGCCAGCGCAGCATCATGCAGGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGCTGGGGTGGCGCTCTTCAAGCGCCAGCGCGAGAAGCCATCTACAGCA
 ACGACTTGCACACCTACATCACCTTCAAGCGCCACCTTCAAGGCCGAGGACAGCA**TG**AGGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCGCTCCCTGCAGGGCTCAG
 TTGCACTGCTGAAGCAGGAGGCCAGGGAGGTCGCCGGGACTGGCATCTTGGGGAGA
 CCTGCTCTCTATCTTGCTGCCATCATCCCTCCACGCTATTTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGACTTGCTGAACCTAAATATTCTAGAACTTCCAGCCTCGTAGCCC
 AGCCTTCTCAAATCTGGAATGTCATGCGAATCACCCGGGGTCTGCTGTTAAATGCAAGATTCT
 GACTCAGCAGCTCTGATGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCACTCTATGAACCACTGGAGCAACCCAGGTCTTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCTCCCCACATTTCTAGAATTTCTCCAAACATTTTTTTTTCT
 TGAGACAGACTCTTGCTCTGTGTCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCCCTCCCGGGTTCAAGCGATTCTTCTGCCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTCTGGCTAATTTTGTATTTTGTAGAGATGGGGTTCCACCATA
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCGCTCGGCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAAATCCAACATTTCTAAATTTCTCTAT
 CCCCCAGGGTCCCCGTGCTATGTTCTTTTACCCCTTCCCCCTCTTCTCTGCTCAGGCC
 TGCACCACTCAGCCACCGTTCATTTATTCATTATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCA
 GTCCAGCCCCAGGGGGGAGAGATGTGTACATAGTTTAAAGCAGACCAGAGCTCATGGGG
 GCTCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGTCTCCTATTACCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCTTCCCGTTCTCTATCCACCTGCCCGAG
 TGCTCATGTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCAGGAGTGTGGGGGCAATTTGGGGGGTGAAGTGGCCCCCGAAGAAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTGCGAGAAGACCTGAGCTCCTCAGCTGGATCCC
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAGGTATCT
 GAACTTCGTTTCTCCAGGGCCTCCAGTGCCTGCCACAGACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCTCATGCCCTCTCACCAGGCCAGTGCCCGGACTCTCCAGGCTTTATCAAGGTT
 CTAAGGCCGGGTGGGCGACTCTCGTCTCAGAGCCCTCCTCCGGCTGGTGGCTGCTTTAC
 AAACAGGCTCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAAGGAGGACCTCAGGCCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCGTGT
 GTTCCCTAGCTTTCCAAACCCAGGTGGCTGCCCTTCTCCCCAGAGGGAGGGCGGCTCCCG
 CCATTGGTGCTCATGCACTCTGGGGTGGAGTGCCCCGGGGGTGATCTCTGTGCTCAC
 AGCCGAGGGAGCCGTGGTCCATGGCCAGATGACGGAACAGGGGTCTGACCAAGTGCCAGGA
 AGACCTGGCTATAAACACCCCTGCCTGATCTGCCCTGCTGACCCGCCAGCCCTGCC
 GTCCAGCATGATTAAGAATGCTGTCTCTTGGAAAAAAGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPGQSGKDGKMGSPGAPCQKRK
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCGCCGCTCCCGGGACAGAAGATGTG
 CTCCAGGGTCCCTCTGCTGCTGCGGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGTGACAGG
 GCTGCCCATCCGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACCTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGAGCTGCCACCCGACACGGTGGGGCTGTAGCTCTTTGAGAAGGGCAT
 CACCATGTCTGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGACGCTCCTGGACCTGTAC
 AGAACAGATCGCCAGCTGCCAGCGGGGTCTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCCGGCGCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCCTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCCGGGCACTGCCCGGCTGCGC
 CTGCCCGGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGAGC
 AGGGGCTCTTCAGCGCTTGCACAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCTCGGGGCTGACGCGCTCGGGCTGGCCGGCAACAC
 CGCATTTGCCAGCTGCGGGCCGAGGACCTGCGCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTTAAGCTCGAGGCGCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTCGGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGGCCCTGAGCTGGTTTGGCGCCTG
 GGTGCGCGAGAGCCACGTACACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCGCCCCA
 AGAACGCTGCGCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGGCCACCC
 ACCACAGCCACAGTGCCCAACACAGGCGCCTGGTGCGGGAGCCACAGCCTTGTCTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGGCCCCAGCGCGCCTCCA
 CTGCCCCACGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACTGCTCCTC
 AATGGGGGACATGCCACTTGGGGACACGGCACCACTGGCGTGTGTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGCTCA
 CGCCGAGGCCACACGCTCCTGACCTTGGGCATCGAGCCGGTGAGCCCCACCTCCTGCGC
 GTGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCTGATAAGGGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTGTGTGTCATGCCCTTGGGG
 CCCGGGCGGCTGCCGAGGGCGAGGAGCCTGCGGGGAGGCCCATACCCCCAGCGCTCCA
 CTCCAACACGCCCCGATCCACAGGCCGCGGAGGGCAACTGCGCCTCCTCATTTGCGCCCG
 CCCTGGCGCGGCTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGCGCG
 GGGCGGGCCATGGCAGCAGCGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAAGTGGAGCTGAAGGTCCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCAACCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCGCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCGCTCCTGCTGCCACACACGTAAGTCTCAGTCC
 CAACCTCGGGGCTGTGTGCAGACAGGGCTGTGTGACCACAGCTGAGGCTGTTCCTCTGGA
 CCTCGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCTACAGTCCCGCAAGC
 CGAGTGCCCTATGAGGACAGTGTCCGCGCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGCTGTGTAACGATGCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCTTGGGGGCGAGTGAAGGAAGCTCCCGAAAGACAGAGGAGCGGGTAGGCGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAACTCAGAGACAAGGACTTGGTTTTTGTAGACAACAGCATGATATG
 AAGGCCTTTTGTAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNIASLPSGVFQPIANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPQPDQCPPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRPLASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNPLLLIAPALAAVLLAALAAGVAAVCVRRGRAMAAAAQDKGVGPGAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAGCCGTGGGGGTTTGTAGCTCAT
 CTTTCATCTCATATGAGGAAATAGTGGTAAATCCTTGGAAATACATGAGAGCTCATCAG
 AAACATTTACATATTTTGTAGTATTTGTTATGACAGCAGGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGGAATCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACGCCAACGCACCTGGATTATCCTATAACCTCCTTTTCACTCAGAGTTCAGA
 TTTTCATCTGTCTGCTCAAACTGAGAGTTTGATTCTATGCCATTAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTAACAAGGAGTTAAGATTAGATTGTCTTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATTCTTCTTTTAAAGACTT
 TGACACCATGCCATTCTGTGAGGAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCAGAAAATTGCTCATCTGCCATCTAAATCTGTCT
 TTTCTAGGATTGAGAATCTTCCCTCATTATGAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAACTGCACATTGTTTTACCAATGGACACAATTTCTGGGTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTGGCATACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGTGACTAC
 TCAAAATCTGTAATGAGAATATAAAATGGAGCATGTACATTCAGAGTGGTTTACATTCA
 ACAGATATAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATATCAAAAT
 CACAATCCGCACACATGCTTTTCCGAATTATCCTACGAAATCCAATTTTAAATTTTGGC
 AATAATATCTTAAACAGCAGGTGTTTAAAAGAATCTTCAACTGCCCTCATTGAAAATCTCT
 CATTTTGAATGGCAATTAACCTGGAGACACTTTCTTAGTAAGTTGCTTTTGCCTAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTATACAAATAAATTTGCTGATTCTGTCTCAG
 GTGCTTGGCCAAAGTATCAAAATCTTGACCTAAATAATAACCAATCCAACTGTGACTCA
 AAGAGACTTAACTCATCTGATGGCCTTACGAGAATAAATTTGCAATTTTCTAAGTTTCT
 CTCCTCGATGCAGTCATTTGAGTAGACTTTGAGTCTGAACTTGAATGAACTGAACTTCATTCT
 CAGCCCATCTCTGATTTTGTTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGGCGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTAAGAAATTTCAATTCAGCTTGAACATATTTCAGAGGTC
 ATGATGGTTGGATGGTCAGAGTTCATACACCTGTGAATACCCTTTAAACCTAAGGGGAAGTAG
 GTTAAAGACGTTTCATCTCCACGAATTTCTTGCAACACAGCTCTGTTGATTGTCAACATTG
 TGGTTATTATGTCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGGTTAGGAAAACAACCCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCATTTATTTATACAGTGAACATGATTTCTC
 TGTGGGTGAAGAAATGAATGATCCCCAATCTAGAGAAGGAAGATGGTTCTATTCTGATTTCG
 CTTTATGAAAGCTACTTTGACCCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
 GAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGGCCACCACAATCTCTTCCATGAAAATTTGATCATATAATTCTTATC
 TTACTGGAACCCATTCATTTCTATGCAATCCCCACCGAGTATCATAACTGAAAGCTCTCCT
 TGAAAAAAGCATACTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCA
 ACCCTTCGAGCTGCTATTAAATGTTAATGTATTAGCCACAGAGAAATGTATGAATGCGACAGA
 TTCACAGAGTTAAATGAAGAGCTCGAGGTTCTACAATCTCTCTGATGAGAACAGAGTTGCT
 ATAAATCCCAAGCTCCTGGGAAGTTGGGGACCATACATCTGTTGGGATGTACATTGATA
 CACCTTTATGATGGCAATTTGACAATATTTATAAATAAAAAATGGTATTTCTCCCTCATTA
 TCAGTTCTTAGAAGGATTTCTAAGAAATGATTCCTATAGAAACACCTTACAGAGTTTATAGG
 GCTTATGGAAGAAAGGTGTTCTATCCAGGATTTGTTTATATAATCATGAAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTGTAATCCCGACCATATGGGAGGCCAAGGTGGGTGACCCACAGGTCFAA
 GAGATGGAGACCTCTGGCCAACTGGTGAACACCTGTCTCTACTGAGTACAGAAATCAAAAATTA
 GCTGGGCGTGATGGTGCACGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCAGGAGGATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCACTGCACTCCAGCTGGT
 CAGACAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCATGGCCCAAAAATAAGGTCTAATTTCAATAAATATAGTACATTAATGTAATATAAATTA
 CATGCCCATCAAAAAAGAAAGGTAGCTGTATTTTCTGGTATGGAAAAACATATAATAT
 GTTATAAATATTAAGTGTGTGCAAAACATAATTTGGTTTGGCATTGAAATGGCATTGAA
 ATAAAGGTGTAAGAAATCTATACAGATGTAGTAACAGTGGTTGGGCTGGGAGGTTGGA
 TTTACGGGAGCACTTTGATTCTATGTTGTGATTCTTATAATGTTTGAATGTTTGAATGTA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPMICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLOHKNDENCSPETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVFCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSI SENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHHNLFHENDSHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTCTTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGACCGGCCCTCGAGGGGTGCGCGGGAAGG
 GAGGGAAGAGGAAGGCGGGGCGGGCCCGCTGCGCCCGCCCGCGGCTCTGCGCGCCCTGTGCGGCCCGGC
 CGAGCCGACGCCAGCCCGCGGGCGGTACACGCGCAGCCAGCCGCGCCCTCCGCGGCCCAAGCGCGCGT
 CTGCTGTGCGCTGCGCCCTTGCCCGCGCCAGCTTCTGCGCCGCGAGCCCGCGCGGCCCGGCGTACGCTGA
 CCTGCGCTCGGCGCGGGCGCGAGCAGG**CATG**TCCCGCCGCGGGACCGCTACCCGAGCTGGCCCTGTTGCTC
 CTGGCAGTGACCTGGCGGGGTCGAGGCCAGGGCGAGCCCTCGAGGACCCTGATTATACGGGCGAGGAGAT
 CTGGAGCCGGGAGCCCTACTACGCGCGCCGAGCGCCGAGCTTCTCTCCGCGCTGCCTCGCGGGGCG
 CCGGGGAGGAGTGGGAGCGCGCCCGCGAGGCCAGGCCGCCCAAGAGGGCCACCAAGCCCAAGAGCTCCC
 AAGAGGGAGAGTGGCTCGCGAGCGCCCTCCACCAAGTAAACACAGCAACAAAAGTATTAGAGAACCAAGAG
 CTCTGAGAGGCTGCCAAGCATGATCACAGTGTCTGCTGGCCGTGAAGATGTCAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCTCCACGGTGAAGCGCTATGGCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGCGGGGATTAAATGAAATGATTTTATGACGGAGGCTGTGCGCGGGAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGGCCCTGACCAGATTCACTGGTGTCACTCAAGGGA
 GGAACCTCCCTCTGGCTGAGTGACTGGTGACATCCTATAAGTCTATGGTGAGCAATGACAGCCACAGCTGGT
 ACTGTTAAGAATGATCTGGAGACATGATATTGAGGGAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGGTGCGCCGCTACATCCGCATAAACCCCTCAGTCTGGTTTGAATAAGGAGCATCTGCATGA
 GAATGGAGATCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACC CGCGGAAGGAGATGACACCACCT
 GATGACCTGGATTTTAAGCACCAATTAAGGAATGCGCCAGTTGATGAAAGTTGGAATGAAATGTGTCC
 CATATATCCAGCAATTTACAAAGATTGGAAGAAAGCCACAGGGGCTGAAGCTGTATGCTGTGAGATCTCAGAT
 ACCCTGGGAGCATGAAGTCCGTGAGCCCGAGTTCCACTACATCGGGGGGCGCCACGGCAATGAGGTGCTGGCG
 CGGGAGCTGCTGCTGCTGCTGGTGAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCTCCACCT
 GTTGGAGGAGACCGGATTACGCTCTCCCTCCCTACCCCGATGGCTGAGTATCAACAAAGCACTTCTCTGATT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAAAGCACTTCTCTGATT
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCGAGGAAGTTCCCAATCACTATATTGCAATCCC
 TGAGTGGTTTCTGTCGGAATAAGCCAGGCTGGCTGCCGAGACAGAGCAGTCAAGCTGGATGGAATAATCCC
 CTTTTGTGCTGGGCGGCAACTGCGAGGCGCGGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGGCTCCCC
 TGGAAAGCAGGAGAACACACCCCGCCCGGATGACCACTGTGTCGCTGGCTGGCTACTCCTATGCTCCAC
 ACACCGCTCATGACAGACGCGCGGAGGAGGTTGTGCCACGAGGAGACTTCCAGAAGGAGGAGGCACTGTCA
 ATGGGCGCTCTGTGCGACACCGCTCGTGGAAGTCTGAACGATTTCACTACCTCATACAACTGCTCGAAGT
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGAATAACCGGGAAT
 TCTGATCTGTTCATGGAGCAGGTTTCATGTTGGCATTAAGGCTTGGTGAGAGATTCAATGGAAGGAAATCC
 CAAACGCCATTATCTCGTAGAAGGCATTAAACATGACATCCGAACAGCAACGATGGGGAATTACTGGCGCCTC
 CTGAACCCCTGGAGAGTATGTGTCACAGCAAGGCCGAAGGTTTCACTGCATCCACCAAGAACTTCTGTGTTG
 CTATGACATGGGCGCACAGGTGTGACTTCACTATAGCAAAACCAACTGCCCAGATCCGAGAGATCATGG
 AGAAGTTTGGGAAGCCCGCTCAGCTGCCAGCCAGCGGCTGAAGCTCGCGGGCGGGAAGAGACGACAGCT
 GGC**TGAC**CTCTCGGCGCTCTGGACCTGCTGGAGCCCATGCAATTAACCAAGCTGGTAGCTGCTACCTAG
 TGGACTCACTCACTGTTGTTTCTCTGTAATTAAGAAAGTGCCTGGAAGAGAGGCTGCATTGAGCGAGCTCC
 CAAAGGGAGAGCTGGAGGCTGAGGCTGTTTCTTCTTGTGCCATTTACCAATAACTTGGACAGAGCA
 CGAGAGAAAGCTGATGGAGTGAAGAACTCAGCAAGCCAACTGGGAATCAGAGAGAGAAGGAGAGGAGG
 GAGCCTGTGCGTTGAGAGCTCTGGCTGCATAGAAAGGATCTGTGTGCTTCCCTGCTTGTGCTGGCAGCAAG
 GTTCCAGCTGCATTTGCAATTTGCAACAGCTAAAATTTGAGCATTTTCCCGAGCTGGGCTGCCAAATGTACCA
 TTTGAGATGCTCCAGCGCTCTTAAGAGAACTCACCCCTCTGCGCCCTGGACATTTGCAAGCTGCTCAAAATA
 ATTCTGTGTTCTTTTGAATAGGCTCATTTGCCAAGTGACATCAGTGAGCCCTTGAATCTGTTTGTGCTCTC
 TTTTAAACAAAGGAGTGTGTCGGAAGGAGAGAGAGGCTGAGATCATTCAGGAGTTTGTGTGGCGCAGAGCA
 TGGAGCTTCTGCAAAATTTCTGGTCCATAAACACCCCGCAAGTCCCTCTGATGCTAGGCTCTGGAGGTT
 CCCCGGTTAGGAGAGGAGAGGTCGACGCTTCTGAAAGGCGAGAAATTTAGCTGGATCTGCTCTTTTAC
 CTGCTAGGACTGGAAAGAGCGAGAAGTGGGTGGCTGAGGCCCTCTCTGCTTGAAGTATTGCCCTGTGTTG
 GAATTGAGTGTCTATGGTTGGCCCTCATATCAGCCTGGGAGTTATTTTGAATGTAGAAATGCCAGATCTTCCA
 GATTAGGCTAAATGTATGAAACCCCTTAGGATTATCTGTGAGCATCAGTTTGGGAAGAAATTTGAATATCT
 CTGCAAGAAAAATGATGCTCTCACTTTTGTAAATGTGCTGCCCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAAGCAAAATGGTAGACCTTTAAAAAAAATAAAAAAAAATAAAAAATAAAAAATAAAAAATAAAAA

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYQGQEIWSREPPYARPEFELETFSPLP
AGPGEWERRPQEP RP PKRATKPKKAPKREKSAEPPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGLNLIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMIF
EGNSEKEI PVLNELPVMVARYIRINPQSWFDNGSICMRMEILGCLPDPNNYHRRNEMTT
TDDLDFKHNNYKEMRQLMKVVNMECPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNDPGYEKAYEGG
SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMWEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRLWLA SYAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHNTCFELSIYVGCDKYPHES
QLPEEWENNARESLIVFMEQVHRGIKGLVRDSHGKGPINAIISVEGINHDIRTANDGDYWRLL
NPGEYVNTAKESGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRGKTROROG

FIGURE 37

CTAAGAGGACAAAGATGAGGCCCGGCTCTCATTTCCTAGCCCTTCTGTTCTCTTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAAATCCCAGCCCCGGCTTCAGCTCTTTCCAGAGTGTGAGCTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGAGCTTAGGCGAGCGGAGGTTCGTGTCCAGTGTGT
 TTCCAATTTACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGCTGGAAACGCTTGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATGACATCAT
 GGAAGAGATACCAATTTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAAAGCTCAGAAATTTGTGACCAAGCTGGAGGTGGAGTAAGAAAT
 ATGACTCTCTTGGTAGAGAAAGCTTGAGACACTAGACAAAAACAATGTCCCTGCCATCCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAGATCAAAAACACCCCTGTCCGTCCACCTCCTCCCACTC
 CAGGGAGCTGTGGTTCATGTTGGTGTGGTGAACATCAGCAACCCGTCTGTGGTTGAGCTCAACTGGAGAGGCTT
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCGAGCATCCAAACAAAGGACTGTATTGGGTGGCGC
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCCTATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAAATG
 GATTGTGGGTATTTATTTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACACACATT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGCTACTATGAACACCAAGACAGAAAGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAAGAAA
 CTTTATGTCTATAACGATGGTTACCTCTGAATTAATGATCTTTCTGTCTTGCAGAAAGCCCCAGTAAAGCTGTTTA
 GAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTCTTCAATTTGAGCAATGTTTAGGTGCATAGTCTTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGTGAGTCTCTTGGGAATCATCTGCTCTTCCAGGCGCATTTTGAATAAAGTCTGTCTAGGGTGGGA
 TTGTGAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTTAAACCTCAGTATGGCGCTAGGGATTCTTTGTACAGGAATAATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCACTAATTTCTCCATGCCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAAATATCT
 GAGACTCTCGAGGGACCAAACTCCAACTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAATTTGGCATGCTTATATATTCTACATCTGTAAGTGTGAGTTTATGGAGAGAGGCCCTTTT
 ATGCATTAAATTTGACATGGCAATAAATCCAGAAAGGATCTAGATGAGGCACTGCTTTTTCTTTTCTCTC
 ATTGTCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATACCTCTCTTCCAAGGCACTCAGAAAGATTAG
 AACCAGCATTACTAACCAAATCCACCCCCACCAACCCCTTCTACTGCCACTTTAAAAAATTAATAGTTTTT
 CTATGGAACCTGATTAAGATTGAAAAAATAATTTTCTTTAATTTTCAATTTGGAATTTTATACATGACTATA
 AGACTATAAGAAAACTGATGGCACTGACAAAGTGTAGCATTTATTGTATCTAATAAAGACCTTGGACATA
 GTTGCACCTTATAGTGTATCAGTTGTGCAATGTAATTTTGGCTTTGTTAAGCCTTGAACCTTTGAAGAAAA
 GAAATTTAATTTTCTTCTAGGACGAGCTATAGAAAGCTATTGAGAGTACTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGTGCTGTATGTGATGCTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCCTTTGAIGTTCAAGTCCCTAGTCTATAGGATGGCAGTTTAATGCTTTACTCCCTTTTAAAAATAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFL LALLFFL GQAAGDLGDVGPPIPSPGFSFPGVDSSSSSFSSSSSRSGSSSSRSLGS
 GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
 QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
 LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGH
 GGVDNISKPSVVQLNWRGFSYLYGAWGRDYSPQHHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
 DLLLYINARELRITYQGSGTAVYNNNMVYNMYNTGNIARVNLTNTIATQTLPNAAAYNNR
 FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
 MFCGVLYATRTMNTRTTEEI FYYDNTNGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG
 YLLNYDLSVLQKPQ

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
217

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

TCTCGCAGATAGTAAATAATCTCGGAAAGGCCAGAAAGAAGCTGCTCCATCTTGTCTGTAT
 CCGGCTGCTCTTGTCAGCTGTGGGACATGCGGGAGCGTCTGGGCGTGTGCTCCATGCGCAAC
 GGATACCAAGTGTGGTGGGAAGTGCCCGTGTTTGCTATGCCGATGCTGCTCACTGGAAAC
 AACTCCACGTGTAACATAGATTATCTAGCACTTTCTGCTTGTTGGAGTATGTGTAGCTTG
 TGTAAATGTTGATACCGGAATGGAGAACCACTGAATAGATTCTTGGAGTATGTGTAGCTTG
 AGAAAGGTTGTGCCCTGTACACTTTGTGGTGCTGCTGCAAGTATGCTTTGTGACGTTT
 GGGTTGGCTATGTTCTATCTGCTCTACTCTGATGATGAAGAGTGAAGAGTAGCAGTGA
 TCTTAGAGCTGCGAGGCACATGGATTTGGTCTTTAAATTTGCTGCGCAATTCGCAATTA
 TTATTGGGGCACTTTCTTCTCAGAAAGCAATTTTCAACTGTGTGGTTTTATGTAGGCAT
 CGAGGTGCTCTTTCTTCTTCTTCACTCAACTAGTCTTACTTATTGATTTGCACATTCAT
 TATGTAATTTGCTGGTTGAAAAAATGAAGAAAGGCAACTCGAGATGTTGGTATGCGACGCTTG
 TATGTAATTTGCAAGCTGCAATTATCTGCTGCTTTAGTTCATGCTGCTGTTCTTTGCTCA
 CTACTCATCCAGCCAGTGTGTTCAGAAAAACAGCGGCTTCATAGTGTCAACATGCTCTCTG
 TGCTGGTGCTTCTGTAATGCTCTATAGTCCAAAAATCCAAGATACCAACCAAGATCTGGTT
 GTTTACAGTCTTCAGTAATTTACAGTCTACACAATGATTTTGACATGTCAGCTATGACCAAT
 GAACCAAAAAAATGCAACCAAGCTCTACTAAGCAATTTGGCTACAATACCAAGACAC
 TGTCCCAAGGAAGGGCAGCTCAGTCCAGCTGTGGATGCTCAGGAATATAGGACATAATTC
 TCTTTTGTGTGTGTTATTTATCCAGCATCGTGATCTCAAAACAATAGTCAGGTTAATAAA
 CTGACTCTAACAAAGTGAATGATTTACAGTAATTAATGAAGATGGTGGAGCTAGAGAATGGATC
 ACTGGAGGATGGGACAGATGTTCCAGCAGCTGTAGATAGTGAAGAGGATGGTGCATCTACA
 GTTATCTCTTTCTTCACTTATGCTGCTTTTCTCGGCTCACTTTTATATCATGATGACCTTACC
 AACTGGTCCAGGATGAACCCCTCTGTGAGATGAAGAGTCAAGTGGACAGTCTCTGGGTGAA
 AATCTCTTCCAGCTTGGATTGGCATGCTGTGCTGATTTGGACACTGCTGGCCACCATGTTCT
 TTACAAAATCGTGATTTTTCAGTAGAGACTTTAGCATGAAGTCCCATTGATTATTTGTC
 TTAATTTGAAACAGTATTTCCCAAGTTTGTAAAGTTGTGATGTTTTGTCTCCCAATGTAACT
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCATTTTGTATTTTCTTACCAA
 GTGATGTTGATATGTGAAGTAGAATGAATTGCAAGGAAAGTTTGTGAATATGGTGTAGATG
 TAGTAAAAGTGGCCATTATGGGCTTATTTCTGCTCATAGTTTGTGAATGAAGATGAAAA
 ACAAATTTGTTTGACTATTTTAAAAATATATAGACCTTAAGCTGTTTTCAGCAAGATTAAG
 CAAATGTATGGCTGCCTTTGTGAATATTTAGATGTGTTGGCTGGCAGGATACGAAAGAAC
 ATGGTTTTATTTAAAAATTTAATAAACAGTCACTTAAATGCCAGTTGTCTGCAAAAATCTTATA
 AGGTTTATCCCTTGATACGGAATTTACACAGGTAGGAGTGTGTTAGTGACAAATAGTGTAGG
 TTATGGATGGAGGTGTGGGTACATAAATGAATAACGAGTAAATATCTACTTTGGGTAGAGA
 TGGCTTTGGCAACAAAGTGAACTGTTTGGTGTGTTTAAACATGAAGATTTGGTTCAGT
 GGAATGTTTGAAGACTCGAAGGATTAGACAAGGTTTGAAGAAAGTAACTCATGGGTTAGA
 AGGAAGTGTTTGAAGAGTCACTTTGAAGTTAGTTTGGGCCAGCAGGCTAGCTCACCTCT
 GGTAAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTCTTAGGCCAGGAATTCAGACA
 GCTTGGCACAAGTGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTTGTGTT
 CAGCACTGAGAGGCTAGTGAAGATGCTGAGGCCAGAGCCAAAGGTTGCAAGTCAGCAAGTCA
 CGTCACTGCTGCTAGCTGGCCAGAGATGCGCCAAAAAATATATATATATATGAGTGAAGTCA
 AGGCCAAAAATTTGACAGGGGAAGGAGTCACTCTTAAAAACAATGAGACATGAATACAGACTTAAATATA
 ATAAATCTAGTCCAGTTCTCTCTTCAAGTTAGAGACATGAATACAGACTTAAATATA
 GCTCAGTAGTCACTATAGGAATATGATATGATTTGATTCACCTCATACTGTGATAAATTAATGT
 AATTAATGTTTGTGCTGTGTCAGCATGACCCATAACAGCTCAGAAGATGATGGAATGTTT
 AGATTAACCTCTGCTTTATAGTATATACACATCAAAAGATGTTTAAATGCTTTTGTAT
 TTATCTGGCAATGAATGAAATATATACATATTTGAACCTTTCAACCTGAAATCAAGCAT
 ATAGAGTTTATGTTATTTGATGTGCTACTAGTGTCTAATGAAGCTTTTAAATCTACAAAT
 TCTCTTTTAAAAATATTTTAAATGTGAATGGAATTAACAACCTTCAGCTTAATTCCCAACC
 TTATTCGTGTGATAGCATTTGATTTCCAAATTTTGAATGGCTGTGTTTTACTCTAAATAA
 ATGAATTCAGAGAAAAAATAAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPNCNILVGYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
EWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGI
VLYVWTLVAPLVLNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAACTAGATTGATCTA
TGCACCTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

123456789101112131415161718192021222324252627282930313233343536373839404142

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTTGGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCGGATTTTTGTGAGAAAGGAGGTTGTTCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGTGCCTTTTGTTCATCCTCATACAACCTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCTGTCTTTGTCTACTACACTCATCCAGCCAGTTGTTGAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGTCTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTGGCCCTGCGATTGAGCTGCGGGTCTGCGGCCGGCGCCGGCCCTCTCCAAT
GGCAAAATGTGTGTGGCTGGAGCGGAGCGCGAGGCTTTCGGCAAAAGCAGTGCAGTGTTCGACAGACGGGGCGAG
TCTCTTGAAAGCAGATAAAAGAAACATTTATTAACTGTCTATTACGAGGAGCGCCGGCGCGGGGCTGTGCG
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGAGAGAAGAAAGCGGAAAAGGAGGACGATTCAC
GTGCTTTCCAGCCAGTGTGACCTGATCGATGGCCCTCTGAATTTATCACGATATTGTATTTATTAGCAGTGCC
CCCTGGTTTTGTGTGTACGACACACACGCTGCACACAAAGGCTCTGGCTCGCTTCCTTCCTCGTTTCAGCTCTC
TGGGCGAATCCACATCTGTTTAACTCTCCGCCGAGGGCGAGGAGGCGAGAGTGTGTGCAATCTGCGGAGTG
AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCAACTTGAGACTCCGCGATCCCAAAGAAACACCAGAT
CAGCAAAAAAAGAAAGATGGGCCCCCGAGCCTCGTGCTGTGCTGTGCTGTCGCAACTGTGTTCTCCCTGCTGGG
TGGAAGCTCGGCTTCTGTGCGACCCAGCCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA
ACATCATCTCGGTGCTGACGGAGCACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCGGGCG
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCTTCGTGACCACACCCATGTGCTGCCCTCAGCTCTCTC
CATCTCACTGGCAAGTACGTCACAACCAACACCTTACACCAACAATGAGAAGTCTGCTCTCGCCCTCTCTGGC
AGGCACAGCAGGAGCGCAGCTTTGCCGTGTACTCAATGACCTGGCTACCGGACAGCTTTCTCGGGAAG
TATCTTAATGAATACAACGGCTCTACGTGCCACCCGGCTGGAGGAGTGGGTGCGACTCCTTAAAAAATCCCG
CATTTTAATACACGCTGTGTGCGAACGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGATTAACCTCA
CAGACCTCATCAACATGACAGCGCTGAGCTTCTTCGCGAGTCCAAAGAAGATGTACCCGCGACAGGCCAGTCTCT
ATGGTCTCATGCGCTTACGACGCCCGCCACGGCCCTGAGGATTCAGCCCAACATATTACGCTCTTCCCAAGCG
ATCTCAGCAGCTCAGCGGAGCTACAACCTACGCGCCCAACCCGGAACAACACTGGATCATGCGCTACACGGGGC
CCATGAGGCCCATCCACTGGAATTCACCAACATGCTCCAGCGGAGCGCTTGACAGCCCTCATGTGCGTGGAC
GACTTCATGGAGAGCATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGATACATCGTTATACACCGC
CGACCCGCTTACACATCGACGCTGAGGCGAGTTGGCTGGTGAAGGGAAATCCATGCGCATATGAGTTGACATCAGG
TCCCGCTTACAGTGAGGGGCCCCAAGCTGGAAGCGCGCTGTGCTGAATCCCCACATGCTCTCAACATGACCTG
GCCGCCACCATCTTGGACATTCGACGGCTGGACATACCTGCGGATATGGACGGAAATCCATCTCAAGTCTGCT
GGACCGGAGGCGGCCGTGAATCGGTTTCACTTGA AAAAGAAAGATGAGGGTCTGGCGGACTCCTTCTTGGTGG
ACAGAGCGAGCTGCTACACAGAGACACAATGACAAGGTGGACGCCGAGGAGGAGAATTTCTGCCCAAGTAC
CAGCGTGTGAAGCGACTGTTGTGAGCTGCTGAGTACGACGCGGCTGTGAGCAGCTGGACAGAAAGTGGCAGTG
TGTGGAGGACCGCACGGGAGCTGAGCTGCATAAGTGAAGGGCCCATGCGGCTGGCGGCGCAGGAGGCC
TCTCCAACTCGTCCCAAGTACTACGGCGAGGCGAGGAGGCTGCACCTGTGACAGCGGGGACTACAAGCTC
AGCTCGGCCGCGCCGCGGAAAACCTTTCAAGAAGAAGTACAAGGCAAGTATGTGCCGAGCTCGCTCATCCG
CTCAGTGGCCATCGAGTGGACGGCGAGGCTTACCACTAGGCTCGGTGATGCCGCCAGGCCGAAACCTCA
CCAAGCGGCACTGGCCAGGCGACCCCTTGAAGCAACAGATGACAAGGATGCTGGGACTTCAGTGGCATCGAGGCG
CTTCCGAGCTACTCAGCGCGCAACCCCTTAAAGTGACACATCTGGTGACTACTAGACAGCAGCAGCTCCA
GTGTGACAGTGGACCTGTGAAGTCTCTCGAGGCTTGAAGACACCAAGCTGCACATCGACACCGAGATTGA
CCCTGCGAGAAACAAATTAAGAATCTGAGGGAAGTCCGAGGCTGAGGAGAAAGCGCCAGAAAGATGTGAC
GTGCACAAATCAGCTACCAACCCAGCACAAGGCGCGCTCAAGCAGAGGCTCGAGTGTGATCTCTTTCAG
GAGGGGCTCGAAGAGAAAGACAGGAGTGTGGCTGTTGGGCGGAGCAGAGCGCAGAGAAAGCTCCGCAAGCTG
TCAAGCGCTGCGAGACAACAGCAGCTGACGATGCGAGGCTCAGCTGCTCACCCAGCAGCAACCGACTGG
CAGACGGCGCTTTCTGACACTGCGGGCTTTCTGTGCTGCACCGCCACCAATTAACAGTACTGCTGGTAC
GAGGACCATCAATGAGACTCAAAATTTCCCTTCTGTGAATTTGCAACTGGCTCTCTAGAGTACTTTGATCTCA
ACACAGACCGCTACGAGCTGATGAATGCAAGTGAACACACTGGACAGGAGTCTCTCAACAGCTACGCTACAG
CTCATGGAGCTGAGGAGCTGCAAGGTTCAACAGCAGTGTACCCCGGAGCTCGAAGACTGGAACCTGATGGAGG
AAGCTATGAGCAATACAGGAGCTTCACGCTCGAAAGTGGCAGAAATGAAGACCTTCTTCCAAATCAGCTGG
GACAACTGTGGGAGGCTGGGAGGTTAAAGAAACACAGAGGTTGACCTCCAAAACATAGAGGACTCACTGA
CTCAGCAGGAGCAATAAACCATTGGGTGATTTCCAGCAGACTGTGCTATTGGCCAGGCGCTGAGAAGAA
AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACCCAGCAGGAGCAGAGATTAATCTCAGGAAGTCC
ATTTTGGCCCTGCTTTTGTGATTATACCTACCACTGCAACAAATGATTTTTCGATTCAAAAGTCA
ACCAATACCCCTCCCCAGAGGCTCACAAGGAAAACGGAGAGAGCGACGAGAGAGATTTCTTGGAAATTTCT
TCCCAAGGGCGAAAGTCAATGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCTCTTATTCTT
TTGGATTTGTCAAAAGAGGAACTAAGAAGCAGGACAGAGGCAACGTTGGAGAGGCTGAAAACAGTGAGAGAGC
TTTGACAAATGACTAGTACGACAAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTGGCTGTGAAGAAA
CTGCTTCTATTATATATGTGACTATTACATGTATCAACATGGGAACTTTAGGGGAGCACTAATAAGAAAT
CCCAATTTTCAGGAGTGGTGGTCAATAAACGCTCTGTGGCCAGTGA AAAAGAAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRNRIRPNIIILVLTDDQDVELGSMQ
 VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTKYVHNHNTYTNNENCSSPSWQAQHE
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
 YSKDYLTDLITNDSVSFFRTSKKMPHRPVLVISHAAPHGPEDSAPQYSRLFPNASQHITP
 SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
 YIVYTADHGYYHIGQFGLVGKGSMPYEFDIRVPPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
 AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
 FLPKYQVRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
 YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAAQ
 PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYIILENDTVQCDDLKYK
 LQAWKDHKLHI DHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRCLKHRGSSL
 HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
 PFCACTSANNNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
 HVQLMELRSCKGYQCNPRTNMDLDGGSYEQYRQFRRKWPEMKRPSSKSLGQLWEGWEG

10
 20
 30
 40
 50
 60
 70
 80
 90
 100

2118 2119

© 2005 Blackwell Publishing Ltd *Journal of Internal Medicine* 258: 11–16

49/330

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQPPWFER
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRRHPRHAR

[illegible]

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCAGAGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTTGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTTGGGACTGAGC
 CCCTGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCTCCTGCAGTGCACTTGTGAGGAAGTGAAGGAGTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGAGGGGAGGAGGGGTTCTGAGGACCTGACTTCCCCTGC
 TCCAGGCCCTTGTCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCAGGGGTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTACCTGGAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCavgSILSEGEESpSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRrvHPALDtyIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSaatLSPGAS
SRGWDDGDTRSEHSYSESgASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTapeK
GKE

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCavgSILSEGEESpSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRrvHPALDtyIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSaatLSPGAS
SRGWDDGDTRSEHSYSESgASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTapeK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCT
GCCCCGCGCCAGT**CATG**ACCCCTGCGCCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCTACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRATIPSHLAYGKRGF
PPSPADAVVQYDVIELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGAAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGCGCTAAATCGGGGGAG
 TGAGGCGGGCGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTTC AACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTGTGTTGTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCCTTGATTAACCT
 ATAAAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAACATTTTTTAGTTTTTAAATATTCGTGG
 TCAAAATCTCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCACGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

100
90
80
70
60
50
40
30
20
10
0

TGGACGGACCTGAAAAAAATGTTTGGATTNTNAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCACCATGAAAGATTCAACCANTCATACC
ATGCGCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGCAA
GTCCGAGGTGATAGTTACAGTGAAGGTGTGTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTGTGGTTTACATGTTGGCCTTTGGATCTCTGATTTGCATCTATGTGGATTCTTTTGGAGGCTT
ATGTTGGTTTAAAGAAAAGACATAGTATACCTGGAATGNTGTATTTTCCAGAATGCCCTTC
ATCTTTTTTGGAGGGCTGGTTTTAAGTTTGGCCGCATGAAGANTATATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCTTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGC GCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTC AACC ACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

2001 100

CGACGCGCGCGT**GATG**TGGCTTCCGCTGGTGTTGCTCTCGGCTGTGCTGCTTCTGGCCCTCTCTGCAAAAGTTACTTCTGGGCACTATCTCTCGGCAAGTCCCGCAATCTTCTTCGGAAGATGTC
AAACGGCCCCCAGGCTCCCTGGTAACTGACAAAGGAGGCGAGGAAGAGTTCATCTCAAGG
TTTTTTCAGCCAAACCAAGTCCGGGAGAGCTGTGATGTGTGGTAAATGGATCTGGTCTGGG
GCGTGGCTGCAGCTGCATTAATCTAGCTAAAGCTGGAAAGAGAGTCTGTTGCTGGG
ACCAAGAGCGAGGGGCTGCTGTCTGACATGCTTGGGAAGATATTTGAATTTGACACAGGAAT
CCATTAACATTGGGCGGTATGGAAAGAGTCTTGGGCGCTTTATCTTTGAGCAGATCACTG
AAGGGCAGCTGGAATGGGCTCCCTCTCTCTTTCATCATGTGATCGATGGAAAGGCGCC
AATGGCCGAAGAGAGTACCCCATGTACAGTGGAGAGAAGGCTACATTACGGGGCTCAAGG
GAAGTTTCCAGAGAGAGGAGTATCATATGCAAGTATAAAGCTGGTGAAGTGGTATCCA
GGGCTCTGATGATGATCTCTGTGAAATCTCTCCATTGGCCGTGGGTGAGCTCTCGAC
GGTCTGGCTGCTGACTCGTTCTCTCTCATCTCAAGCATCCACCAGAGCTGGTGA
GGTCTCCAGCATGCTGGGGCTCTCTCTGAGCTCAGGCAGTACTACGTACATCTCCCCA
CTTAGCGTGTACCCCAACACAGAGTGCCTTTTCCATGCAGCGCTGCTGTGTAACCATAC
ATGAAGAGAGCGCTTTTATCCCGCAGGGGGTTCAGATGAAATGGCTTCCACACCATCTCCGT
GATTACGGGGCTGGGGGGCTGCTCTCAAGAAAGCCACTGTGCAGAGTGTGTTCTGGACT
CAGCTGGGAAGAGCTGTGGTGTCTCAGTGTGAAGAAGGGGCATGAGCTGTGAAACATTATTCG
CCCATCTGGTGTCTCAACGCGAGGAGTGTTCACACACCTATGAACACCTTGTCCGGGGAAGCC
CCGCTGCGCTCGAGGTGTGAAGCAGCAACTGGGGACGCTGGCGCGCGGGCTTAGGATGACCT
CTGTTTTCTATCTGCTGCGAGGACCAAGGAAGACCTGCATCTGCGCTCCACAACACTATCT
GTTTCACTGACAGCGACATGGACAGGCGGATGAGCGCTACGTCTCATGCTCCGCCGGGAAGA
GGTCTCGGGAACACATCCCTCTCTCTTCTTCTGCTTTCCATCAGCCAAAGTATCGAGCTGGG
AGGACCGAATTCGAGCGCGGCTCCACCATGATCATCTGCTCATACCCATGCGCTACGAGTGGTTT
GAGGAGTGGCAGCGGAGCTGAAGGGAAGCGGGGCATGACTATGAGACCTTAAAAACCT
TTTTTGTGAAGCTCTATGTCTCAGTGTCTCTGAACATGTTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTACCAACAGTCTATCTTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGTACCTTGGCGCGCTGCACCCTTGTGTGATGGGCTCTTGGGGC
CCAGAGCCCCATGCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGTGTCG
GGGCGCTGCAAGTGTGCCCTGTGTGTCAGCAGCGGCCATCTGAAGCGGAATCTGTACTCAGAC
CTTAAGAAATCTGTAATCTTAGGATCCGGGCGACAGAAGAAAAGAT**TAGT**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCATTAATGTCTCTG
CATTAGTTCTCTGCAGCTATAAAGCACTTAATTTGGTTCTGATGCTGCTGAAGAGGCGCTG
TTTTAAATACAAATTCGGAATCTGGGGCAATTGAATATAGTATGAGTGGGAGGCTGAT
TCTTTACGCCCTTTATAACATGCCCCATCTCTATATAGATATTGCTAGCTGGGAGGCTGAT
TCTATGACGAGCGGGCTCTGTCATCTGCGCATCTGCTCTCACTCACTGATATCTGATATCT
ATCATTTCACTGTGGATAGAACATGACCTGCGCATCTGCTCTCACTCACTGATCAAGCGCA
TGCTCTGAGGCTCTGATCTATCTTATTTAGTGTCTACGCTGCACAGTCTACACTGTCAAGG
GAAAGGAGGAGTCTTGAAGCTTTAACTCAAACAACTGGCGCTGGTTTGGTGGCCATTCCATA
GCTTACAGCTCTAATCTCTTTTGTGCTGGGTTCACTGGCTCTTCAAGGGACAGGAAT
GCTGTGTGGCCAGTGTGGTTCTGGAGCTTTGGGTTACAGCAGGATCCATCATGTAGTA
GGGTGCATGTGACATGATCATCAATTCATATGGAAGTCCGGGCTGCTCTTCTTATCA
CTGGGCTGGCAGCTGGTTCTCAATGTGCCGACGGGACTCAGTACTGTAGGCTCAATCAAGC
TCTATCCACAAATACACAGGAAGGTTGATGCAAGGAAGGTTGACATCAGGAGTCAGGCA
TGGACTGTAAGATGAATATCTTGTCTGGGCTGAAGCAGGCTCAGGGGCAATCCAGGCCAAGG
CACAGCAGGGGACGTGACGGAGGAGTTGGGTGAAGGAGGGAATCATACAGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCGAGAAATGGCATTTGCGATTAATAGCACATGTAGGG
TTAGACAGGTAGGTGAATTCAGAGCTCAAGTTTGGAAAAAGACTTTTCAGTTATGTCTTTG
GTATCAGACATACGAAGAGTCTCTTTGTAGTTCTGTGTTAATGTAACTTAATAAATTTATTTG
ATTCATCTGCTTTAAAAAAAATAAAAA

FIGURE 64

MWLPLVLLLVALLLAVLCKVYLGFLSGSSPNPFSEDKRPPAPLVTDKARKKVLKQAFSAN
 QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSFFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVSSGAPHAILLKFLPLFPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
 GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPiVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYVYYDDTMDQAMERYVSMPEEAAEH
 IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
 SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
 PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTGGCACCGGCCCGGAGAGGAGGATGCGGGTCCGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGTCTGCTGAGCTTGGCCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTCTAG
 AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAGAAAAGTACGGAAACCAGCTTGT
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAATGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAAGGCTCTTGTAT
 ATTATACATTGGAGCTCTTGGGGCAATCTAATAGCCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTGTGGTTTATAGCGGCCACAACTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGAGTCCACA
 ATTTTCTTTTAAATGATTAGTTTGGCTGATTGCCCTTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAATGACTCCAGAGAGCTCTACTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCATTTATTGTAGTGACACTGTGCCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACTCATTTTATAATAA
 ATTTATGCTAAGATTAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
EPCHFPPFLFDKEYDECTSDGREDEGRLWCATTYDYKADEKWGFCETEEEEAKRRQMQEAMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFKEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

CTTCCAGCCCTGTGCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCC
GCTCCCTGCTCTGGCCATGGCCTGCCGCTGCCTCAGCTTCTCTGATGGGACCTTCT
GTCAGTTTCCAGACAGTCTTGCCACAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCCTGCTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCCTGTCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCCTCCCCTCTGCCTCCCATTCT
GCCCCGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

68/330

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTTISPVQPEDDADYYCSVGYGFSF

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

FIGURE 69

GCGGCCCGCCCGGAGACCGGGCCCGGGGGCGCGGGGCGCGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGCACGCCGCGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGCCCC
 CCGCGCGAGGCTCCGGACGCGGAGATGACGCCGAGCCCCCTGTGCTGCTCTGCTGCCG
 CGTGCTGCTGTGGGGGCTTCCACCGCGCGCGCGCGCGGAGGCCCGCCCAAGATGCGGGGAC
 AAGGTGGTCCCCAGGTCGGCCGGCTGGGCCGACCTGCGCGCTGACGTGCCAGTGGAGTGA
 GGGGACCCCGCGCGCTGACCATTGTGGACCAAGATGGCCGACCATCCACAGCGGCTTGA
 GCGGCTTCCGCGTGTGCCCGAGGGGCTGAAGGTGAAGCAGTGGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCTCTGCTGT
 GCTGGATGACATTAGCCCCAGGGAAGGAGCCTGGGGCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTACACAGCCCTCCAAGATGAGGCGC
 CGGCTGATCGCACGGCCGTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCCAGCGGGCACCC
 TCGGCCCCGACATCAGTGGATGAAGGACGACAGGCTTGAAGCGCCGAGAGGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGAGGACAGCGGCAATAC
 ACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTATCCA
 GCGGACCCGTTCCAAGCCGTGCTCACAGGCACGCCACCCGTGAACACAGCGTGGACTTCG
 GGGGACCACTCTTCCAGTGCAGGTGCGCAGCGACCTGAAGCCGCTGATCCAGTGGCTG
 AAGCCCGTGGAGTACGGCGCCGAGGGCCGCGACACTCACCATCATGATGTGGGCGGCCAGAA
 GTTGTGGTGTGCTGCCACCGGGTGACGTGTGCTGCGGGCCGACGCGCTCTCACTCAATAAGC
 TGCTTCACTACCCGTCGCGCCGAGGACGATGCGGGCATGTACACTTGCCTTGGCGCAACACC
 ATGGGCTACAGCTTCGCGACGCGCTTCTTACCGTGTGCTGCCAGACCCAAACCGCCAGGGCC
 ACTGTGGCCTCTCTGCTTCCGCGACTAGCTTGGCTGCGCTGGCCGCTGCTTCTGCGATCCAG
 CCGCGCTGTCTTATCCTTGGGACCCCTGCTCCTGTGGCTTTGCCAGGCCAGAGAAGACGCC
 TGACCCCGCCGCTGCCCTCCCTTGCCTGGGCACCGCCCGCGGACCGCCGCGACCG
 CAGCGGAGACAAGGACTTCCCTGCTTGGCGCGCTTACGCGCTGGCCGCTGGTGTGGGGCTGT
 TGTACCCCGCTGGTCTCGGCGACGCCCGCAGCACTTACTGGCCCGAGGCCAGTGTGCTGGC
 CCTAAGTTGTACCCCAAACTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACACTCACAGCTGGAGGGCAAGGTCCACAGCACATCCACTATCATGTCTAGACGGCACCGT
 ATCTGCAGTGGGCACGGGGGGGGCGCGCAGACAGGAGAGCTGGGAGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGACCCATGGCGAGGAGGAATGGCCAGACCCGAGGCAGTCTGTGTG
 TGAGGCATAGCCCTGGACACACACACACAGACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACAGCTGCTCCCTGAAGGCACACGTACGCACACGATGCACAGATATG
 CCGCTGGGCACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGCATGCCAGAAAC
 TACAAGGACATGCTGCTTGAACATACACACGCACACCCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACACGGATATGCTGTCTGGACGACACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCCCTTGACACACACATGCACGG
 ATATTGCTGGACACACACACACACACACGCTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGACAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGCAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTACACACACACGACAGATATGCTGTCCGGACAC
 ACACACGATGCACAGATATGCTGTCCGGACACACACACGACGACGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTCACACACGTCAGATATGCTTGGACACACACA
 TGTGCACAGATATGCTGCTGGACATGCACACACGTCAGAGATATGCTGTCCGGATACACAG
 CACGACACAGATGACAGATATGCTGCTGGGCACACACTTCCGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACACTCACACACGTCAGATA
 TATTGCTTGGACACACACATGTCACAGATATGCTGTCTGGACATGCACACACAGTGCAGATA
 TGTGCTCCGGATACACACGACGCACACATGCAGATATGCTGCTGGGCACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCTGGACACACGACAGTGCAGCTGCTTTGG
 GAGGGTGTGGCGTGAAGCCTGCAGTACGTGTGCGCTGAGGCTCATGTTGATGAGGAGCTTT
 CCGTGCTACACGCTCACTCCCCAACTCTGCCCGCTCTGTCCCCGCTCAGTCCCCGCTC
 CATCCCCGCTCTGCCCCGCTTGGCGGCTATTTTGGCACTGCTTGGGTGGCCAGG
 AGTCCCCCTACTGCTGTGGGCTGGGTTGGGGGACAGCGAGCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTATGGGCTCATCCCCAGTGCAATTTCCCCCTGACACAGAGAAGCGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGAAGAGCTGGGTTGCAGGGAC
 TGTGCTCTCTCTCGGCGCGGGACCGCGCTGGTCTTTCAGGCATGCTGATGACCCACCCCC
 GTCCAGGCCAGACACACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAAATTTTA
 TGTAGAGTTGAGCTGAAGCCCGGTATATTTAATTTATTTTGTAAACACAAAA

FIGURE 70

MTSPSLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSWWSRFRVLPQGLKVQVEREDAGVYVCKATNGFGSLSVNYTLVVLLDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLP
TGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

ACGAGCTGAGGAGCCCTGGTAAAGACAGGTCTCACTTGATGAGAATCTCCACGGGGACATCTCCAGAGT
AGTCATCTGTGAAGACCCACATCTACTTCTTGCCACTTCCACGGGCTTGGGGGAAAGATGTTGGGGACAC
AGGCCTGGGTGTCTTCTCTCTGGTCTCGGAAGTTCACATCTGTGTGGGGAGACACAGATCGTCACCCACT
GTATGAAGAGATGCTCCAGCTGGGAGAGAGAACCCAGCACTCTTGCCAAAGCTGCCGACCCCTGGAGACCCCT
TGAGTGGACACACATGGTTCACATCGACTACCCAGCGGGGGAAGGGCAGATCTGAGCGGCTGACAGCCATTCGCT
TCTACTTATGGGACGGTGTATGTCGCCCTCCCTGGGCTGAGAGCTCGGCACACTGATGCACATCTCGGGCG
GAGTGGAG
GAACTCTCTTAATACACGTCAGCTCTCTCTGCCACAGATCTCTTGGCCGAGACACAGGCCATCTTGA
GCCCATGTCTCCTTGAGCAAGTGTCTCAGTCTGCTGTGTAGCTGGGTTCAGACTTCGACATCGACACGCAAT
TGTGGGACAGATGGTGTGCTGTGCTGAGCTGAGGCACGGAAGAGGGTTCAGCATCTCATGTGGCCAGGACTGTACAG
CTGTGACCTGACCTGCCCAATGGGCCAGTGAATCTGACTGTGATGGCTGATGTGTGCGAGGACTTATGCTT
ATGGGGCTGTCTCCCTCCCGGGAGTGGCCAGCTGAGGGGCTGCTATACCTCCCTGACACAGACAGCCAGT
GAGTGGAG
GATCAACAAGAGTCAAGTCTTCCGCCATCTGTACTCAACAAGCCACAGACTCTGAGGACGCCACCATCAAGG
CAGAGTGTGTGAGGGCAGAGACTTCATCAATGGTGTGAACCTGTGACCAAAAGCCAGGAGACTGGGCAGCC
GTGTCTCTGTGTGCTTAAGGCCACAGGAAGGCCAGGCCAGCAAGTAATTTTGGTATCATATGACATATCTGCT
GGATCTCTCTCTCTCAAGAGATGAGGAGCAAGCTGGTGTGTGAGGAAGACTGCAGACAGCCAGGCTGGGGAGTCT
TTTTCAGGCGCCAGAGTATGCTCGGGGCTTGAGTTCAGAGTTCGCACGTGATGTGCACAGATCTGTATGAT
CTTCTCTACTATGAGCTGGGACGCTGCCCTTTTAAGACTTTGTGAGGACGAGCAGATTAATGGGATCAGGTGCGGT
ATCTGTGTGCAAGTCTGTGGCACTTCCAGACAGAGGAAGGAGACTTCAGTGCAGTGTGCTACGCTACCC
ACCAAGGTGGCCAGGAGTGCAGCTGCAGCGGTTGACGGAATCTGGAGCAATCTGGAGCGCGCTGTCACTGTG
TGTGACATGAGGAGGAGCCATCGCTTGTGGCCATGTGTACATGGGGAACGCGCTGTGAGGATCAGTGGGTACA
AGGCCAGTGGGAG
GAGTGGAG
CTTGGGAAGAGGCCATCACTTTGGAGGCATGGAGAGCAATCATCCCTCGGGGGAAGTGTGTGTTGAAGCC
CCATGGTGTGAATGGAGATTCATCCGAGATTTCTACAGGCAAGTGGGAGGCCCTCATAGGAAGAGTGAAG
GCGAGTGTGACATCTCTGGATCCCGGAAATTTTCCACAGCCAGCTGCCAGACTGACCTGAAATTTCTATCAAT
TGACGAGGAGGACATCTTCCCTCTCGGACGTATGGCAATCTCTCTCTGTGGAATTCAGAGATGAGTCACTCT
CTGAAATCTGTCTCACTCAATACAGACAGGGCTTGTGGGAGGAGGAGTGATTTCTCAATTTGAAATCAAG
GGAGAACAAAGAGAGGACAGAACTCTCTGTGGGCAAGCTTGGAATCTGTGAGGAGGAGCTTTTAACTGG
ATGTTCTTGAAGAGAGCGGCTGCTTTGTTAAGTGTAGGGCTACCGAGTGTGAGAGTCTTGCTGCTGTAGGAC
ATCCAGGGGGTGTGATCTTCGGTGTATTAACTCGGAGCTGAGACTGGCTCTGTCTCGAAGCCATGGGCGCTGGGG
TCTTGTGAGTGTCTATCGAGGCCCTAAAGCGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CTTATGAG
CTTAAATGAAATGAGCTTCCCTCGAGCTCTATCAACAGCTCAACTACCGCTGGAGCGACCATGAGGATCCAG
GGTGTAAAAAGACGGCTTTCAGATTAGCTGGCCAGGCCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCA
TGTATGCTTTTGAGAACCTCCGGGATCTGTGAAGGAGCCACCCAGCTGCAGCCCATCTCCGTTCTACAGGAT
GAGGGGTGCTGATTAAGTACACACAGCTGCCCTTCAAGAGAGTACGCTTATGAGTGCAGTACGAGATATCT
TATGAG
ATGTGCTGCTCCGCAATCAAGGCGGACCTATCGGCGGACATCTGGGAGCTTATGGAATCCGAGATGTGAGG
AGCATCTGGGACAGGAGGACCGCCAAATGTCTCAGCTGCGCTGTGTGGATCTCAAGTGCAGTGGGATGCTTATG
TCAGGACGCTGTGGACCGACCTCTGTGGAAGGTCACTCCCGAGGGCAGCTGCCCTGCAGGCCATGTGAACCCCA
TGCTGATGATGAGTACCTGTGCAACCTTGCACATCTGCAGTCAACACGACAGCAGGTGAGTACACATCTGCTGGCA
CTCTGAGCACCTGAG
CGCGCTGAG
CTTACCTTCAACTGTGTAGAGAGGCAAGTAGGCCCGCAGAGTGCTTCCAGTACCTCCAAGACCCCGAGCCGAC
TCCCTCTCTCGAGGACCTGTCCAAGGAGAGTCCGCTCGAGGAGGACGACAGCGGACGAGGAGCGGTGGCCAGC
CCAGGCTGGAGTGTGTGSCCTCTTGAGATTTCTAGATTTGCTCAAGAGCCCTGATCACTAAAGTTTGTGTG
ACTTCAACCTCTCTCGCCCTTATTCATGTGACAGCGATTTGTGAGACTGATGTCAGCAAACTGCTACTTGGT
TTAAGCACTCTGTTTCTTGATATCTGTGTGTTTCTTCTGACCTTATCTATTTGTCAGTCTGAGGAGGAGGAG
CGCGCTGAG
GGCCATCTGTAAATCTCGAGCTTCAGTGTCTCAATGTCTCAITTAATGCCATTAATGCAAAATACTTCTCTTCT
TCTTGGCTGGTTTGGCCCACTCGAATGTGATGTATCTGTGCTGAAGATCAAAATAACCAATATAAGCATAT
TCTTGGGCTTGTCTCCAGGACATAGGCAAGCTTGATCACTATGTTATCATATTAAGTTGGTGTGAATAAAG
AATAAAGCAACAATCTTTACTGAAATGAATAACTTATTTCTTGTGTAATTTGGATTTGAGTCTGAGTGG
GAG
ATCCAACTTAAGGAGGTGTCTAATCTATTTGTGATATCTCCCTTTCGATTCGCTTTGCTTGTCTGACAAAC
CAGTGTAGCCACAGGCGAGATGTCATAATGATCATCTGTATTTGCAAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVT SVLGRQTMLTQSVRRVQPGKKNP SIFAKPADTLES PGewTTWFNI
 DYPGKG DYERLDAIRFY YGDRVCARPLRLEARTDWT PAGSTGQVVHGSPREGFWCLNREQ
 R PGQNC S NYTVRFLCP PGSLRRDTERI WSPWS PWSKCSAACGTG VQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLT CPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQT DSDGRFRIPGLCPDGK SILKITKVKFAPIVLTPMKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPD KYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNC GISKTEEREIQCSGYTLPTKVAKECSCQRCTETR SI VRGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEI PSRSFYRQNGEPYIGKV
 KASVTFLDPRNI STATAAQTD LNFINDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKVKVLH
 DSTQVKMEPHISTVKLWSLNPD TGLWEEEGDFKFENQRNRKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKV RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLAS LAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
 VKKTA FQISMAKPRPN SAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN
 EDDPM SWTEDYLAWWPKPMEFRACYIKVKI VGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAA CLEFKSGMLYDQDRVDRTL VKVI PQGSCRASVNPMLHEYL VNHLP LAV
 NNDTSEYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGS SRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACCTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGATTTGTCAGAGTCCCTGTGATTCATG
 CCGTTTGGGTTACGGTCTCCTCAGTGTGCGAGCCCTACCCCTTGGTTGGGGACATTTGATTTGGTTAAGACT
 CAGATTTACACGGAAGAAGGGAAGTTTGGGATTTACATGGCTGCCAGCCGAATTCACCGCATGACAAAATA
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTCTGAGACCTCTGTGCAATGGGCAATC
 CCTACATGTGCAATATATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGGATTTT
 GAAGGAAGCATCCCTCCACATTTTGGCAGCTGCCACTTTGGAAGGAGTATCCCAAGCCTCTCCAGGTTACAT
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGCTCCAGACC
 AAATGATCCTGGGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCAGCATACGGCTCTTAGAATCATTTGACACAGA
 AGAGTACTCAACAGGGTATACAACAAAATAGCAAAATATCCACTTTGAAATCAAGACAGGTTTCGGCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTCAAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGAAATATTTGTAGATGAGTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCAACAACACTACAGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGTACGAATGTCTGCGACAACAGAGCTCCTGCACTGCCAGAACGAGGAGCGTGCCACA
 ACAACGTGCGCTGCTGTGCCCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGGCCGCCGCAACGGCACCCAGCGCTGCTGCTGCTGACACGCTGCT
 GGGAAACGGCAGCCCTGCTGTTCTAGGTTGTCACCTCCAGCCACACCGGACGGGCGCTGTGCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGATCAAGACTGTTAATTT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCAGATTTGCCAGCTGACAGCATATTGTGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAACAAATCAACCGACTAAAAACATTGGC
 TACTCTAGCTGGTGGCCCTAGTACGACTCCGCCAGTGTGGACCAACCAATAGCATTTCTTGTGCTCAG
 GTGCATTGTGGGCATAAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTCCGCTCCTGAATCCCTTCAAC
 CTGTGCTTTAGTGAACGTGCTCTGTAAACCTCGTTGGTTGAAAGATTTCTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACAGCCCTCTAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCCACTATACAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCTTTTGTATTCAAAATGAAGTT
 ATTTTCTTGAACCTACTGTAATATGTAGATTTTTTGTATTATGCAATTTGTGTTACCAAGCAATCTGTTAAT
 GTATCTAATGCAATCAGCAAGACTGACATTTTATTTGTCTCTTTCGTTCTGTATTGTTTCACTGTGCGAGA
 GATTTCTCTGAAGGCAACGAACTGCTGGCATCAAGAATATCAGTTACATATATACAGAGTGTAAAGA
 TTCCACCAAGGCAATCTAATGTTTCTTGTGCTTTAAACACTGGAAGATTTAAAGAAATAAACACTCCTGCA
 TAAACGATTTCAGGAATTTGATATGCAATTTCTTAAGATGAAGGAACCAACCAACGACTTTTCACTCACT
 TACTGATTTCTGTGTGGACTGATACATTTCACTGACGATTTAGTCCAGGAAGATGGATGATGTTCACT
 AGCTTGGCAACTTCTGCAAAATATGAGACTATTTCCACTTTGGGAAAAATTAACACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
 VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK
 EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
 HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
 TTKKLRFDDFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
 SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
 CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
 PLVF

12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGCGCAGCGCCGACTTCCGAAGGCCGCGCTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCCACTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCTGTGGTGGGAATTCACAGCTTCTCATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACTTGAGGAGCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCACACATCATGTGTGCTGCCCTGAATCT
 CATTCGAGGAGTTCACCTTGACAGAACATTTCTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAGGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCATGTCAAGTAAATCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAACAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAATAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGCATTGAAACGTGAGCGCGA
 CCGGACCTTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCTTTAAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTTCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGCGGGCGGGCGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGT**A**
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCAACACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTTGGCAATTGCCTGGGTGCTGCTCTGCTCTCGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTCCTCTCCCAACCTGTCCCTCA
 TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTGTCTGGCTCCAGAAAG
 GGTGTCCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCACTCTCCTTCCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGTCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTCTGCTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAGCTGGGCTCCTTTGG
 TGCCGTCACTCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTTGGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCTGCGGCCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCTCTCTTAAGCTCAGCACTTCCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCGAGCCTTTGCGAGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCCTGCCCCG
 CTCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCACT**TGA**CCTCCAGCTGGGGGTGGGA
 AGGAAAAAAGTGGCACTGCCATCTGCTGCCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATTT
 GCATAATCTGAGCCAGAGTTTGGGACAGGACCTCCTGCTTTTCCATACCTAACTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGTAGTGCAAT
 AGGGTGGGGTAGGGGAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCCTCGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK
IALELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMFVSTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSLGSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCCLKVTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

79/330-1190

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCACAGAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTGCAACACTGTACATCTCTCCACAGATCTTCTGACCCGCTTC
AAGAAGCCTGCTGAGTTACACACAGCTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTG
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTT
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGAGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCTAGTCTGCTGT
GGGTGATATTACTGGTCTGGCTCCTGTCAAGGACAGTTTGAAGGACACCCAGGCCATT
ATTTTCTCCAGCTCCATGGACCACAGTCTTCAAGGAGAGAGTGTACCTCACTTGCAA
GGGATTTCTGCTTCTACTACCACAGAAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCTGGGCTCAAGTGATCTGCTACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCTGCTGATCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTACAAGAA
TGATAATGTCTTGGCATCTCTTAATAAAGAACTGACTTCCAAAAAAGAGAGAGAGAGAGAGAG
AAA

83/330

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

0000722.4400

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCA**ATGGCT**CCCGAGAACCTGAGCACCTTTT
 GCCTGTGTGCTGTATACCTCATCGGGCGGTGATTGCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCCTCTATAAAGGATATTAAGGCGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAC TAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGTATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGAGAGTG**
 AATAAAATGGACTTTGTTTTAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTGTTTTATTTCATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACAAATATAGAGGGTTGGA
 GTTGTGTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYVAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVVCDECPNVKLVNEERTLEVEIEFGVRDGM EYPFIGE GEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCGAGTCGCGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTGTCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCTGTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCTCCGTTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGACG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGTGAGGAGCATTGGAAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**TGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTTGAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTGAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTATTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAAGTTGATGATTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACCTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVIRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

000072014900
000072014900

FIGURE 89

GCTTCATTTCTCCGACTCAGCTTCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATTGGTTTAGAAAGAACATTGAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
 GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
 AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCGTCTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCACATGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTNGNCNAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFVFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVFVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCTTCTGAGTCCCTGGATCTTTCTTCTCTTGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCTCAGGGCTAATC
 ATCAACACCATTTCAGTCTTCACTCTCCTCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCAAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGC GCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGAGACCTCCGGGACTACCCCGAGAAGTATTTTTCCT
 GATTCAGTGTGAGGGCACAGGTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAAGGGGTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGTGTATATGACTGTACACTCAATTCAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAAATACCATGCAGATTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGC TCGGCCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGA
 GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCCTCGTGAACCTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCTTTTCTTCCAGTTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGTGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
 AACCCTTGGTTGCCAGAGATAAAGTGAAGTGTCTTATAGTGAGATGACTAAATATGCCTC
 CAAGAAAAAAAATTAAGTGTCTTTCTGGGTCAAAAAAAAAA

Figure 1 consists of 12 diagrams illustrating the stages of a cell's division. The diagrams are arranged in two rows of six. The top row shows the cell starting as a single circle, then elongating and pinching in the middle. The bottom row shows the cell starting as a single circle, then elongating and pinching in the middle. The diagrams are labeled with numbers 1 through 12.

Figure 1 consists of 12 diagrams illustrating the stages of a cell's division. The diagrams are arranged in two rows of six. The top row shows the cell starting as a single circle, then elongating and pinching in the middle. The bottom row shows the cell starting as a single circle, then elongating and pinching in the middle. The diagrams are labeled with numbers 1 through 12.

FIGURE 94

CTGAGCGCGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGTGTTTTA
 TACAATTGACATTAGAAAATATATCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAAACAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGAACATTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCAAATTCGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGACAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTCACCTTTCCTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAATGAAAAAGCAAGAAATAGCCTTAT
 TTTCAAATATGAAAAGAAATTTATATGAAATTTTATCTGAGTCATTAAAAATTCCTCTTAAG
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGVEVKGAEAKNSITDSQMDDEVVYITIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFERLLHKNLQEH
FSNQDLVFLLLTPSIITFESCS¹THRLHLSLYKPKGLFHRVPLV²ANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSI³CKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKS
CNYNNHLDVVDNLTLMVEHTIDPEASFASTFQCI⁴KKHALDLDRRWQFKSRLLDTQDKRSKA
NTGSSNODAKSSKSSPTEDEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGGCGGAGGCGAGAGTCAGCCGAGCCGAGTCCAGCCGAGCGAGCGGACAGCGCAGGCGCAGC
 CCAAGCAGCGCGCAGCGAAAGCCCGCGCGCCACACCCCTCTGCGGTCCCGCGCGCGCTGCCACCTTCCCT
 CCTTCCCGCGGTCCCGCGCTCGCCGGCCAGTCAGCTTGCCTGGTTCGCTGCCCGGAAACCCGAGGTCAACCA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGGCACC
 GGGGACCGTTCCTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGGTCTCCTCCGCTTCTGCTCTTCCAC
 CAACTCCAATCCTTCTCCTCCAGCTCCACTCGCTAGTCCCGACTCCGCGACGCCCTCGGCCCTGCCGTAG
 CGCCGCTTCCCTCCGTCGCCAAGGTGGGAACGCTCCGCCCGCGCACCAAGCACGGTTCCGCTTGGC
 CGCGCTTCTCTGCACCTTGGCAGTGTCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTCGCACGCTCTTACGTGTCCAAGGCTTCAACAAGAACGATGCCCGCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGGTTTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAGTTTG
 ATGAATTCCTCAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGCCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATGAAGCTCCAGGTTTACTCGTGCTTTTGTAGCAGCCGCTACTTTTCGCTCAAGGCTTACGCGTTGCGGG
 AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCCGAGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGCTCTGCTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGTCTCTTTCAACATTGAATCGCTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTTATGAACATCGAGG
 ATAATAGTCTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTTCCATCTCTCAAGTGCCTTCAGTGTCTGCTTCAGACCCACATCAACC CGAGGAACGCCAACCCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATCTGCTCCT
 CCCTTCCGACAACTGTTGCAACGATGAGAGGATGGCTGCAAGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTTGCAGTGACAGGAATGGATAGCCAAACGAGGCAACCCACAGGTCCA
 GGTGACACCGAGCAACCCAGACATACTGATCCTTCTGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCAACAAATGGGACGACGTGGACTTCTTTGATATCAGTGATGAAAGTGTGGAGAGGAATGGGAAT
 GGCTGTGAGTATCAGCAGTGCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA
 GAAAGCCGACAGTGTGGTGTCCGTCTGGGGCACAGGCCCTACCTCCTCACTGTCTTCTGCTATCTTGTCTCTGG
 TTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTCTGAGAAAAGTTCATCAAAAAGTTAAAGGCACCAAGTT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAGTGTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAAGGCACTGTGCATTTAGTTGGT
 TCTTGCTCCCCCAACCACTGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTACTTGTGATTTGTGA
 TTTTCTCATCTATATTTGTTGTATGTTTCTTCTCATTCGTTTGTGGGTTTCTTCTCAACGTGATCT
 CGCCTTGTCTTCAAGCAACAGGGTCCCTTCTGGCAGCTACATGTACGTATTTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEMLNDFWARILLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRLKQLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGCQPPKPLPAGRISRISISAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCCATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
 AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
 GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
 CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTGTTGTTGCTCTC
 TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

AATGGCTGTCTTAGTACTTCGCCGTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGCATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCCTCAGGATTAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAAAA

101/330

FIGURE 101

MAVLVLRLTVVVLGLLVLF LTCYADDKPKDPDDKPDGKDPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
2211
2212
2213
2214
2215
2216
2217
2218
2219
2220
2221
2222
2223
2224
2225
2226
2227
2228
2229
2230
2231
2232
2233
2234
2235
2236
2237
2238
2239
2240
2241
2242
2243
2244
2245
2246
2247
2248
2249
2250
2251
2252
2253
2254
2255
2256
2257
2258
2259
2260
2261
2262
2263
2264
2265
2266
2267
2268
2269
2270
2271
2272
2273
2274
2275
2276
2277
2278
2279
2280
2281
22

FIGURE 102

GGATGCCACGCGCTGCAGAGGCTGAGCAGGGAAGAACCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCCGACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCCACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCGCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCATCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGTCTCCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCTTTCATGTGCGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTGAAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGAAGTGTCTCCCAACGTTTGCTCCCAATGTTGTCT
CCTTTCTTCTGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT
CTCTAGGAAGTGGTCAAAAAGTTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCCACTACCACTTCTTCTGAGCTGGGGGCCACAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAAATATTTTTTAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGP HIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIY LPLRGT

103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTCTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAA
 AAGTAAAGGAGGATCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCTCTACTAAAGTTGTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCTGAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCTGGAGTTTTTGTGCAAACTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAAACAGGCAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTGAACTGTAAGCAAGCATTTCACAG
 GAAGTCTCGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTGAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCACGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

CGACGCTCTAGCGGTITACCGCTCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCTGCGGC GCGGGCGCTGAGCTGGCAGGCGGGT CGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGGCAGCCTTTGAGGGGAACGACT
TGTGCGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAAGAAAAGATGTCAATT
CCGTAAAGTAAACATCATCATCTTGGTCTCGGGCTGTTGCTCTCTTCTTACTGTTTTGCAC
CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATT CAGGAATTGTAG
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCTGTGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
ACAGCATTTCAGCAACAACCTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCTTAACTTTTGAAGGAAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCG
ATGAAACCTTTAACTTTGCAAGGTTCTACTTGCCATTCTGGGTTCCCGACGCAAGAAGCG
CCATATACATCGGATGATGATGTAATTGTGCAAGGTGATATTTCTGCCCTTTACATACAGCA
CTGAAGCCAGGACATGCAGCTGCAATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
TTCTGAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
CTGACGGAATGGAACGACAGAAATATAACTAACCACCTGGA AAAATGGATGAAACTCAATGT
AGAAGAGGGGACTGTATAGCAGAACCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGTTCCAGT
GCTGGA AAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTGGGGAAAAATGGTATATTTCCA
GACCCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGA AAAAGATGTGTGTCAGCTAG
GTAAGAGATGACAAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
ATGTCCTCATCTGCCTTACCAAGTGT TTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAAATAAAACTTACATTTTCAATAGTTAAAAA AAAAAA
AAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTCTGCCTGTCTATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTCTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCAG
GCTGGGCCCTCCCCCTGGTCTCCAGTGTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAAA

109/330

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPWSLEPRT

Figure 1

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCTCCAAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGA
 TCA**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCAACACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTGTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAATCACAAATAAGCCATCAGCAGTGCTCCCTTCTGCTGTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGCCAAGTGAATATAAGCCCTT
 TTCGGGCATTCCGTACATGTGGTGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAAATGACTATAGCTGGGGCAGTGTTTACTTGTATTTCACAGAAGT
 AAAAAATGATCCTCCTGATCATCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTCTCTGTGTTTGTCTGTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAGGAGCAACAAATTAACAATGCAAGGGCAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTAAAAGACCTAATAAACCTATTCTTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFIAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC
PAGCQDPKYHVYGT DVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGV TYP SALTYS SSKSPAAQAGETTKAYQRPPIPGTTAQPV TLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHR SQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGA AFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPAT HFNLKTH TNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGA AE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKT LQPLVKRVCDTDR LACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTK EFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD I
LNAIKRVGYWGGTSTGA AINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQE ELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

1991 1992

CAGGATGAACCTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGCACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCCTCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCACTACAGTTTTCTCTGACTCTAAT
TGATGCATGGACACCTTGCTGATTTGGGGAATGTCTCAGAATCCAAAGAGTGTTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAGGCTGGGGTGGAAAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCCTCTCCTGAGAATGGCTGAGGAGCGGGCCGAAAACCTCC
TCCCAGCCTTTGACAGCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTTCATGCGGTG
AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCTGAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGGTGGCCAGGACCGCAGGCATCGGGCTGGCTGGACCTCTCACTTTGAGTACTTTGGT
GAAAGGAGCCATCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT
GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
CTTCGGCCAGAACTTATTGAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGAT
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAAACCACTTCATCCACAACAATGG
GTCCACCTTCGACGCGGTGATACCCCTCATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTTACTCTCTCAAACGGAGCAGGTG
GAAATTTCAAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
CTTCTCAGCTGCCCGAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
AGACTCCTCAT**TA**ACCACCTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAACTATAATA
AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
 VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
 LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
 RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
 AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
 GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
 FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
 IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGFWEPPARPGT
 LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

AAGGTTCACATTTTCTCTGGAACTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGT
 GAGATGGACAGAAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGGTTTTCT
 ACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGCACCTAGAAACACTGGAGCCAGGGGCTGCATATGTGTGAAGGCCGACA
 CATCTTGTAAGGCCATTGGGAGGTACAGCGCCTTGAGCCAGACAAGATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTATCTGGCCCTGTTTGCCCTTTGTTGGCTTCATGTGATCCTGTGT
 GGTGCTGCCACTGTTCTGCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAATAAACAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCTAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTCT
 TGTGGTAAAGTACAGAATTACGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQTS AW
SILKHFPN RNSTILTRPGMEITK DGFHLVIELEDLGPQFEFLVAYWRREP GAEEHV KMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACACCTTTTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGCAACCCCTTGCGCGCAAGGG
GTTNCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**TGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCGCGCGCAGCAGGAGCAGACTTCTACGACTTCAAGCGGG
 TCAACATCCGGGGCAAACCTGGTGTCGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCAACTGTGTGAGTGAGGAGGTGAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTT**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCACCTGTGTGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTCTTATGCCATTGGTCCCATCATTCTGTGGGGGAA
 AAATTTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAAACAAAAATGTGTGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCTTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAAATCCA
 AACAATACCTCACGATATAAAAATAAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

10
20
30
40
50
60
70
80
90
100
110
120

FIGURE 121

CGGACCGCTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTGCGGATGC
 TGGCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCGGGCCGCCCTCTCT
 CGGAGTTGGCAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTTCAGGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCTAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCAGAAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCCTGTCTGCCATG
 ACCCCATCAACATCCAGTTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTTGCCCAACCCCTGTACCATGTGCTGGGTTCCTGGTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCATGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCTGTATGGTACCCCCAGCAT
 GTTCGTGGACATTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATTGTGTGGAG
 GTGTCATTGTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCTATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTGCGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCAATTTTCAGGAAAGATCCAGAAATTCAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGCGCTGTCTGGCCGGTTGGCCT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTATGCACCTAGATGTCCCCAGCACCAGATTCT
 TGAGCCAGGCACATCAATGTCAAGGAATTGACTGAACGAATGAAGCTCTCTGGATGGGTG
 CGGGAAGTGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTTCCCTGTCTGTCTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGLTLLLDVVAAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPPQKTEEAVDQDKWYWTGDTVAT
 MNEQGFKIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
 TGATCCTGCCCCAACCCCTGTACCATTGCCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG
 ATGTACGGTGCCACCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
 CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
 ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
 CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
 TGCTTATGGAACACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
 AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
 GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
 CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGATCAGGACAAGTGGT
 ATTGGACAGGAGATGTCGCCAC

98

Author	Year	Country	Sample Size
...

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQLQCCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRCVQDEFCTR DGV TGP GFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPPEPTT
VASTTSVTTSAPVRPTSTTKMPAPTSQTPRQGV EHEASRDEEPRLTGGAAGHQDRNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 126

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHVDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRLLEPLDANVDA

0000723 111000

FIGURE 128

AACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCACT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTTCCATCCAAA

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAATCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTACCCACCACTATTTAAGGTCCCTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATC
TTCATATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCGATGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCCCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGGATCTAACTCCTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCTCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCATATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAACTGAACATAAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCTATGGGGTTTATGAAAAATACCTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAGAGGCCAATTCATGAGTAATTATTGCAATTGGATT
 TCAGGTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLLFLLPSAQGRQKESGSKWKVFTDQINRSLNENYEPSCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRLGLTHYQITKNRLYRENDCMFSPRCSGVEHPILEVIIGRLPD
MEMVINVRDYPQVPKWEPAIPVFSFKTSEYHDMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKKYLFNFGRGVAASFRFKHLFLCGLSVHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELQFVKKANDDDVAQEIAERGSQFIRNHLQMDITCYWENLLSEYSKFLSY
NVTTRKGYDOIIPKMLKTEL

Figure 1 illustrates the steps of the proposed algorithm for finding a minimum spanning tree. The process starts with an initial graph (a) and proceeds through a series of edge selections (b-l) based on the minimum weight rule, resulting in a final minimum spanning tree (l).

FIGURE 134

CACCCCTCCATTCTCGCCATGGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCAGGAGTGGAGTTCTGTCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTATGCGGTACTGGGAGCC
 CATACCCCAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAATCCACCTGCTCTCTCGGCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACCTCCCCCTGGCACTGTACTTGCCTCTGCGCCTCAGGGTCCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFVTSRPLRGGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLLVFGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLAFLLLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCAGTGAATCC
 CTCAAATGGAGCCTCTGCTGCTGCTACTCTGAGTTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGAAGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCATATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCTTTCAAGGTGTTCCCTCCATCTGCAGTGGGTTGGGTTATATAA
 TGTCAGAGATTTGGTGCCAGGATCTATGAAGTGTGGGTACGCTAAAACCCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAAGTGAACATTCATATTCAGAAGA
 CACAAATCTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCTGTAGACTAGAATTTCTTAAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTTATTG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDII RQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLNLNLHSEKFFTGYP LIDNYSYRGFYQKTHISYQEYFFKVFP PYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

0000723-11902

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCATGATGACACAACA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTICIVHKMNKEVMPSIQSLDALVKEKKLQGKPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAATCGTGTGAGAAATGACTTTGAAAGCATTGCTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCTTAGTATTAAATTCCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTGTGTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**AATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGATGGAATCCAGCCCTTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCITT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGGCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAAGTATTAGGATTTGATTTCTTGAAACCCCTCA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCATTTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGG

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAGCAAAGGGATT
GAATCCGGATGGAAGCTCCAGCCCTTTCAACCCCTGGGTGGATTTTCTCC

100
90
80
70
60
50
40
30
20
10
0

FIGURE 143

GGCACGAGGCGCTCGTGCCAAAGCTTGGCACGAGGGGTGCACCGCGTTCTCGCACGCGT**CAT**GCG
 GGTCCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAAGAAAGACGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTCGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCTCGAGCTGGGCGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGCCAAGCTGGCTATCCGCGTG
 GGA CTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCGCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTCCGAGGACAGACCCATGCTGCAGTTTCTCCTGC
 ACACCAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
 TTCCTGCACACGCCCGGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCGCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCGCTCATCCTCACCCCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA
 GGCTCT**TAG**CTGCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCGTGTCCCAGCTGCAAGGTGGGGCCGACTCCCC
 GCGGTTCCCTTACCACAGTGCCTGACCCGCGGCCCCCTTGGACGCGCGAGTTTCTGCCTCA
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGTGTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLETTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLSDSA
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVS LQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCCTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCTCATACCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATTTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTACAGAAAGTGGCCAGGAGAAATCAGCACACTGCTCGGAGAAATGAGG
 CGCTTCTGTGCTGGTCTTGCCCTTGGCTCAGTCTCTGCTAACTACATTGACCAATGTGGGCAACCTGCACCTTCCCTG
 TATTACAACTCTGTAAGAGTGCCTCCCACTACGGCCCTGACCAAGATAGGAAGAGGCGCTCACAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCAGAGGTTTCTGAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTGCTACGTGTCCTCGGACAGGAGCGGGCAGCCAGCATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCAGCGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGCCAGG
 GCAGGGAAATCTGAAAAACCACTGCCCCGTAAGTCTTTCCAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGATAGATCCCAGTGAAGCCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCTCTCACAACACGCTGTGCGTCTCCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAAGTTCGCGAGCAGGAACAATGGACAGGCC
 GGTGCTCAGACACCCGAGATGACAGCTTTATGTGATTTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTTGGCATATCGA
 CATGGTCAGCTTGGAGGAGATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TCGGGCTCATCTGATTAGGCCAGTGAAGACGTGTTCACTCGTGTGTCGCCAGGTTGGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGTGGTCCCCAGGGCCAGGGGAGGAGGACACAT
 CCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTCTCATGTTTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTGCATCGACA
 GAGGTGAGCCGGAGTGAGGCAGTGGCATATTGAAAGAACATCATCTCGATAGTACTCAAGCTTTTGAAGT
 CAAAGAGTATGAGCCCGAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAAACACATATGGCCCCACCA
 GTGACTGGTCCCCATCTGGGTGATGTGGTGGAAATTACCACGGTGTCTGTATTAATCTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCAATTTAGGAGGTTATGAAGAATCAATGGAACAAACCTTT
 TTTTCATCAATCCATTTGTTGAAGGAACACAGCATACAATGATGGAAGAAATAGATGTGGTATATTCTCTCTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGTGTCAGAGACTGCTGAAAGAACTTAAGGAGGA
 ATTACTCTAATATTGTTTCTTGGCTGGCAGCTTTTATTAAGATCAATGATGGGTGAGAGAAAACAGAAAAA
 TCACAAATAGGCTAAGAGTTGAAACACATATTTATCTTGTACAGTTTATATTTAAAGAAAGAAATACATTTG
 AAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATATGATTCAAAAAAATTA
 AACTCTAGTTTCTTTTTCAGTGTGGAGATTTCTCATTTACTCTACACATTTGTTTATATTTTCTATTCAAT
 AAAAGCCCTTAAACAACTAAATGATTGATTGTATACCCCATGAATCAAGCTGATTAAATTTAAAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTACATTTATGCCCATTTTAATTTACAGCTAAAATATTTTAAAAATGCA
 TTGCTGAGAAACGTTGCTTTTCATCAACAAAGAAATAATTTTTCAGAAAGTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPEVSAAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SELSIRLVGGSETPLVHIIIIQHIIYRDGVIARDGRLLPGDIIILKVNMGDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHLIQASERRVHLVVSQRVQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTDGILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSPPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

147/330

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTGAAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTAC
CCATTGAGAAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAAATATAAATGCTGTATTATA

GGACAGAGCCAGGAATAGGAGGTTCTACTGCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCAG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCACAAAGTCTGGAAGTTTTCCCCAAA
 GCCGTGGGTGCTCATAAAGTCTGTGCACCCAGCCACCACGCCCATCACCTATTCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCT
 CCACCTCAGGTGCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCAAGGTTGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCTTCTCTGCCG
 AGCCAGACATCGGACTGGTCTGGTGCCAGGCTGCAAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
 GCCCATCTGTGCTTGGCTGCTCAGGAGCACCCGCCGTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGAGGTGAGAGGACGCAAGACAGCCACTG**TAG**ATGAAC
 GTCCAGAGAGCCAAGCAGCGCAGAGGACTGACGGCCATCAGCGTGCACTGTTCTGATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAATAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCGAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA
 CTTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGGAAGAAA
 CTAAATGTCACAACGGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTACAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCTT
 TTGCCAACAAATTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTAAATTTTAAATAAGAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPLGKKLNVTAWKAQNPVLEVVLDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAATGGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGACGCAAGGGACC
TTAGATAGGCTTATTTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTTCATTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATG**AAG
 CTCTTGTGGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGGCTCGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCAGAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTGAATACCTGTCTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTACGCCCTGATTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGTGGAACCT
 CAACCTGGGCCCAATAAACCTCTCTTCTTTGCCCATGACCTCTTACCCCGCTGAGGTACC
 TGGTGGAGTGTGACTCTACACCACAACCTTGGAACTGTGATTGTGACATCTCTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTGATGCTCCCAT
 GCACATGCGAGGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCAATGGGACAGTGCTCAGCCACGC
 CTCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGC
 TTTGAGACACTGGGGGTGACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTCTA
 CCACGTCCACTGGTTACCAGCCGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCCACAATTC
 ATGACCATATAACTACAACACCTACAACACAGCATTGGGGGCCACTGGACAGAAACACAGC
 CTGGGGAACCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTCAGACCCA
 TACCAGGACAAGGTACAGGAACTCAAAAT**TGA**CTCCCTCCCCAAAAAAGTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTTGTA
 TATGCTTATATATTAAGTCTATGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYLNLGMCNIKDMFNLTPLVGLEELEMNGHFFPEIRPGSFHGLSSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT VTVVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATD TTDKMQTS LDEV MKTKIIIGCFVAVTLAAAMLIVFYKLRRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHDHIN YNTYKPAHGAHWTE
NSLGN SLHPTVTTISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLTDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSNVLSGNEKRTCQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPH
QLYSAAFSKQKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWEPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLCEEQHEDHGIPVSVTDNMFCAWSEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTGGGTGGGCCACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCTTTCTGTGCTCTCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTGTTCCCAACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGGTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGATGGGGAGGCCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCATTGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAAGCTGTTACAGCTCATTTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTATCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGCAGCAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLIGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVYIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDWFVGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CGTGGGCGGGGTGCGGCAGCGGGCTGTGGGGCGGCCCGGAGGAGCGACCGCCGAGTTCT
GAGCTTCCAGTGCATTCCTCCCGCTCGCGCCACGCTTCTCCCGCTCGGGGCGCCGATAGG
GCCAGGAGAGTGTTGTCGCCCTCGCGCGATCTGTGGCTTGCTGCTCTCTGCCCTGGG
CCCGGCGAGGGGTGGCCGCGAGGCGCTGTATGAATCAATCTACCAACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGCGCCAGCCTGGTGGCCAGGACAACGGAGCCCTGGCCCTG
CCCGCTGACGCCACCTTACCGCTTTCACCTGGATGGATCCACACCCCGTGGTGGCTTACTGGCAA
GATGGAGAAGGGTCTCAGCTCCACATCCGTGTGGTGTGCCACAGCTGCCCGGGAAATTCGCCG
TCTGTCTTGGGTCTACTGCCGTGACTGTGGATGTCCGAGCTGTGGCCAGGGGTTTGT
GTCTTCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTCAACCCAGAACACTTCTCTTACC
TGTCGCCACCTCTATCTCATCAAGACCGTTCGAAAGTCTCTCTCTCTCTCCACGACCCGA
GCAACTTCTCAAGACCGCTTGTTCCTTCTACAGCTGGGACTTCGGGAGCGGGACAGCATG
GTGACTGAAGACTCCGTGGTCTATTATAACTATGACTCATTCGGGACCTTCAGCTGTGAAGCT
CAAGTGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
CCGGGGACTTCTCCGCTCGCTGAAGCTCAGGAAACCTTCGAGGATCAAGAGTGTGGGG
CCCACTCTAATCAGACCTTCCAAGAAGATCAGCTGACTGCACTTGAATCTCTCGGGAGGCCCTCC
TGTGACTGTGTGCTGGGCTCTCAAGCTGAGTGCTCTCCGCTGGAGGAAGGGGATGTGCCACC
CTGTGTCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTCGGGGACTAC
TGCTTTCAGCATCCGGGCGGAGAATATCATCAGCAGAACACATCAGTACCAAGATCCAGGT
GTGGCCCTCCAGATCAGCGCGGTGCTTTGCTTTCCCATGTGCTACATCTATAGCTGTGA
TGTGGCCCTTCAATCATGTACATGACCTCGGGAATGCCATCAGCAAAAGGACATGTTGGAG
AACC CGAGGCCACCTCTGGGCTCAGGTGCTGCTGCCAGATGCTGTGGGCTTTTGTGCI
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACACGGGCTGCTCCGCGCCCTCT
ATAAGTCTGTCAAACCTACACCGCTCGAGCAGCTCCCTCCCCACCCCATCTCAGTGTAA
CTGACTGCTGACTTGGAGTTTCCAGCAGGCTGGTGTGCCACTGACCGAGGGGGTTCATT
TGCCTGGGGCTGTGGCGCTGATCATCCATCTCATCTGTACAGTTTCAAGCACTGCCACAAGCC
CTCTCTCTCTGTCAACCCCTGACCCAGCCATTCACCATCTGTACAGTCAGCCAGCTGACA
TAAGCCCATCTCGGTTACACCCCTTGACCCCTACTTTGAAGAGGCTTCTGTCAGACT
TTGATGCTTGGGCTGTTTCGCTGTGACTCTAGTGGGCTGGCTGCCACTGCCCATCTCTCT
CTCATATTGGCAGACTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTA
CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATGGGCAAGCTCACAGAGAGAAGTGTGATGTATACACACACACACACACACA
CACACACACAGAAATATAAACACAGCTGCATAGGCAATTCAGATGATCAGCTCTGTA
TCTGTTAAGTCGGTTGCTGGGATGCACCTGCATAGAGCTGAAAGGAATTTGACCTCCA
AGCGCCCTGACAGTTTCTGGGCGCGGCCCTCCCTTTTGCTTTGTCTCTGAGTTCTTGC
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGCCGTGATGGGGGGCAGGACT
AATACGTAGTGTATGAGAGTGCTTTTATAAATACAGCTTATTTTATCGAAACCCATCTGTG
AAACTTTCACTGAGAAAGGCCCTTGCAGCGGTAGAAGGTTTGTAGTCAGGCGCGGGCGCG
TGGCTCAGCGCTGTAATCCAGCATTCTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
GATCGAGACCCCTGGCTAACACCGTGAACCCCGTCTCTACTAAAAATAACAAAAAGTT
AGCGGGCGGTGTGGTGGGTGCTGTAGTCCAGCTCATCGGAGGCTGAGGAGGAGGAATG
TGCGCAACCCGGGAGCGGAGCTCTCAGTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
GTGACAGAGCGAGACTCTGCTCTCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCTATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCGTCCCCTCCCTTCCTTATTTATTCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTTGTTCCTTTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

63
60
58
56
54
52
50
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0

165/330

FIGURE 165

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

000072011900

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCCAAACTCTACATGAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAAGGAGAAGAACCACAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCCGATCTGCGTGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTCAGAGAGCCATGGTGAAGCGCTG
 CCCACACGCTCTGTTTGAAGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAGTTTGGAAATTGGAGCCACAGTTTACCC
 TGTGCTATCAAGTATGACCCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGGCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGTC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCCAC
 AAGGACAGGAGCCGCTCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCCGCCAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCAAACCGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACGTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAG
 CTTGGAGCTCTGCAGACATATAGGAAGGAACTGTCTATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTTTATGCTGCTGCTGATGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCCTGAACCTCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAAATATGAGTCGGGGG
 GAGTGGTGTGATTCTTACCTCACAGGCTGTGTGGGGATTAAGAGTGTCTGCGGGTGTGAGTGA
 AGGACACATCACGTTTCACTGTTTCAAGTACAGGCCACAAACGGGGCACGCGAGGCTGAG
 CTCAGAGCTGCTGCATGGGCTTTGGATTTGTTCTTGTGAGTAAATAAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSABEELESWNLLSRNYNFQYISRLTVLWGLGVLI RYCFLPLRLALAF TG
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVIIASDGYIAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGVL D LLWDGGLKREKV KDTF
KEEQQKLYSKMIVGNHKDRSRS

00
10
20
30
40
50
60
70
80
90
100

FIGURE 168

GCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCCCTGGGCTCCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTAAGGAGTTGAATCAGGCCGTGCGGACGCGGCGGAG
 GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG
 GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACACAG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
 GGGACAAGCAAGGAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGAGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

169/330

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGI AIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHF PFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLP PWKTL LLLAPGEFQLSGVGP

0000722.14190

FIGURE 170

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCTCCATGGTCTCCTGTGTCTCCTGTGTGGTGCCCT
CCTGCTAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGAAAAATCCCCACTCAC
TGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAAATGTTATC**TAG**ACAGCAGTG
CACTCCCCTAAGTCTCTGTCTCA

MAGSPTCLTLIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVLT
IQPEGGTIIVTQNRNRERVDFPDGGYSCLKSLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLVPLLLSLFVLGLFLW
FLKRERQEYIEEKKRVLDICRETPNICPHSGENETDITPHNRTILKEDPANTVYSTVEIP
FKMENPHSLTMDPTPRLEAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCCACATAC
AGCCAGAAGGGGCACCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGTGCTGCTGATGACCAGATTCCCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAA
ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAAATCCCCACTACTGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACCCCTTGACAAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCCCTTGCACTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Figure 1**
 12. **Figure 2**
 13. **Figure 3**
 14. **Figure 4**
 15. **Figure 5**
 16. **Figure 6**
 17. **Figure 7**
 18. **Figure 8**
 19. **Figure 9**
 20. **Figure 10**
 21. **Figure 11**
 22. **Figure 12**
 23. **Figure 13**
 24. **Figure 14**
 25. **Figure 15**
 26. **Figure 16**
 27. **Figure 17**
 28. **Figure 18**
 29. **Figure 19**
 30. **Figure 20**
 31. **Figure 21**
 32. **Figure 22**
 33. **Figure 23**
 34. **Figure 24**
 35. **Figure 25**
 36. **Figure 26**
 37. **Figure 27**
 38. **Figure 28**
 39. **Figure 29**
 40. **Figure 30**
 41. **Figure 31**
 42. **Figure 32**
 43. **Figure 33**
 44. **Figure 34**
 45. **Figure 35**
 46. **Figure 36**
 47. **Figure 37**
 48. **Figure 38**
 49. **Figure 39**
 50. **Figure 40**
 51. **Figure 41**
 52. **Figure 42**
 53. **Figure 43**
 54. **Figure 44**
 55. **Figure 45**
 56. **Figure 46**
 57. **Figure 47**
 58. **Figure 48**
 59. **Figure 49**
 60. **Figure 50**
 61. **Figure 51**
 62. **Figure 52**
 63. **Figure 53**
 64. **Figure 54**
 65. **Figure 55**
 66. **Figure 56**
 67. **Figure 57**
 68. **Figure 58**
 69. **Figure 59**
 70. **Figure 60**
 71. **Figure 61**
 72. **Figure 62**
 73. **Figure 63**
 74. **Figure 64**
 75. **Figure 65**
 76. **Figure 66**
 77. **Figure 67**
 78. **Figure 68**
 79. **Figure 69**
 80. **Figure 70**
 81. **Figure 71**
 82. **Figure 72**
 83. **Figure 73**
 84. **Figure 74**
 85. **Figure 75**
 86. **Figure 76**
 87. **Figure 77**
 88. **Figure 78**
 89. **Figure 79**
 90. **Figure 80**
 91. **Figure 81**
 92. **Figure 82**
 93. **Figure 83**
 94. **Figure 84**
 95. **Figure 85**
 96. **Figure 86**
 97. **Figure 87**
 98. **Figure 88**
 99. **Figure 89**
 100. **Figure 90**
 101. **Figure 91**
 102. **Figure 92**
 103. **Figure 93**
 104. **Figure 94**
 105. **Figure 95**
 106. **Figure 96**
 107. **Figure 97**
 108. **Figure 98**
 109. **Figure 99**
 110. **Figure 100**
 111. **Figure 101**
 112. **Figure 102**
 113. **Figure 103**
 114. **Figure 104**
 115. **Figure 105**
 116. **Figure 106**
 117. **Figure 107**
 118. **Figure 108**
 119. **Figure 109**
 120. **Figure 110**
 121. **Figure 111**
 122. **Figure 112**
 123. **Figure 113**
 124. **Figure 114**
 125. **Figure 115**
 126. **Figure 116**
 127. **Figure 117**
 128. **Figure 118**
 129. **Figure 119**
 130. **Figure 120**
 131. **Figure 121**
 132. **Figure 122**
 133. **Figure 123**
 134. **Figure 124**
 135. **Figure 125**
 136. **Figure 126**
 137. **Figure 127**
 138. **Figure 128**
 139. **Figure 129**
 140. **Figure 130**
 141. **Figure 131**
 142. **Figure 132**
 143. **Figure 133**
 144. **Figure 134**
 145. **Figure 135**
 146. **Figure 136**
 147. **Figure 137**
 148. **Figure 138**
 149. **Figure 139**
 150. **Figure 140**
 151. **Figure 141**
 152. **Figure 142**
 153. **Figure 143**
 154. **Figure 144**
 155. **Figure 145**
 156. **Figure 146**
 157. **Figure 147**
 158. **Figure 148**
 159. **Figure 149**
 160. **Figure 150**
 161. **Figure 151**
 162. **Figure 152**
 163. **Figure 153**
 164. **Figure 154**
 165. **Figure 155**
 166. **Figure 156**
 167. **Figure 157**
 168. **Figure 158**
 169. **Figure 159**
 170. **Figure 160**
 171. **Figure 161**
 172. **Figure 162**
 173. **Figure 163**
 174. **Figure 164**
 175. **Figure 165**
 176. **Figure 166**
 177. **Figure 167**
 178. **Figure 168**
 179. **Figure 169**
 180. **Figure 170**
 181. **Figure 171**
 182. **Figure 172**
 183. **Figure 173**
 184. **Figure 174**
 185. **Figure 175**
 186. **Figure 176**
 187. **Figure 177**
 188. **Figure 178**
 189. **Figure 179**
 190. **Figure 180**
 191. **Figure 181**
 192. **Figure 182**
 193. **Figure 183**
 194. **Figure 184**
 195. **Figure 185**
 196. **Figure 186**
 197. **Figure 187**
 198. **Figure 188**
 199. **Figure 189**
 200. **Figure 190**
 201. **Figure 191**
 202. **Figure 192**
 203. **Figure 193**
 204. **Figure 194**
 205. **Figure 195**
 206. **Figure 196**
 207. **Figure 197**
 208. **Figure 198**
 209. **Figure 199**
 210. **Figure 200**
 211. **Figure 201**
 212. **Figure 202**
 213. **Figure 203**
 214. **Figure 204**
 215. **Figure 205**
 216. **Figure 206**
 217. **Figure 207**
 218

FIGURE 176

MTCCEGWTSCTSCNGFSLVLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
 IPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNPSNSNA
 NCEFSCLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSDNTMASGWRASSFHDSEENKHL
 IHFSVFLGLLLVGILEVLVFLGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTGGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

20111222 11:00

ATCCGTTTCTCTCGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAAC TGTGAC **ATG** GAGAGAGTGACCTTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCAATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGTG **TGA** GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCTCTAACACTGGCCCCAGCACCTCCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGCGAGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTC
 TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAAACTGCCCGGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCACAGGGCTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCCGCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATGCCACCATCTTGAGCTCAGTGCCTTTGTAGAGAAAA
 GAAGCCAGCATATCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG
 CACCTCCCACTCAGGATATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGTCTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCTTAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAATGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTCTGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGA
GTGACTTTCTGACCATCCACCTGTTTTTTTGAGATTGTCATGAATAAACGGTCTGTCAAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWG
HLGLITPTEBGLKDSQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGLLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDVIDVLLSKDEDEG
KALSDEDIARAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

182/330

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC
AGTGTGGAGAAAAACTAGGCAAACACACCTGTTTATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTCACAAAAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

2014-07-22 14:00

FIGURE 185

GAACATTTTATGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240

FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPHQVRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADKO

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGCTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCTTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGCGGCTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACAAGA
 GCCTCCTTGTTCATAACCACAGGTTACCTACAAACCACTGTCCCCACACAACCTTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLEYYVNPPEPTPGARVFVPRVRMCSGASPRSEIMDKKGSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

GGAGTGCAGATGGCATCTTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGTCTTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCTGTGCGAGAAAGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGA
CCGGTTCTCCTTCGGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGTTCCCTCCCTCCCTCCCTGGGGCTTTGTGGCAAAAATCCTA
TGGTTATCCCTGGGAACGAGATCAGCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
ACTAACAGACTTGCTACTCACTGGGAACCTGCTGTGGGCTCAAATGAGCGCCTTTGCTG
CTGTTTCTCCTGTGCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTACCCACCTTCA
ACACGTACACCAGGATGGTGTGGAGTTCAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAAC
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCTCGGCGCTGTCAAGTGCAGCCCCAC
CGTGGGTCTTTGACCAGCTACCACAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
AAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
TAGGCTTGGCCCTGCTTTACACGTCGTCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGTTTTTAGGCTCTACGAATAAAGCTATGAAATAGGGTTATCTTTAAGTC
CTAAGGGATTCTGGGTGCCACTGCTCTTTTCCCTCTACAGCTCCCATCTGTTTACCCAC
CCCATCTCACACATCCAGAATTCCTTCTTTTACTGATAGTTTCTGTGCGAGGTTCTCGGC
TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGVTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSQEVVQYNWETGDDRFSRFSRSGMWLSCSEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPFPLLCGKNPMVTPGNADHLHRTSTHQL
PPTNRLRLATHWEPCLLWQATERLCCFLCPVRSPDGGGPHDVFSTLSPSDCQLGSRRLLETTCLE
LWLGLHLGLHALHLLHGVGCHHLQHVHQDQAGVGOVA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCTAGCTTTGGCCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCCTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCTAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTCA
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTCCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCTGTCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAAACAATAAAACAAATTTCTTAACACTGAAA

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCGCGCCCTCGGGTCTGGAGCGCAGGAGCGACGTCA
 CCGCCATGCGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGTATGCTT
 GGATGTGGCCCTTCCAATATACAACAAATACCTGCCCTCTTTGTTCTATTTTTTACATCCCTTCAACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAAGCCTTTGTAAGGAACTTGCCATCTTTC
 TTACAACGGGCTTGTCTGCTCAGCTTTGGACTCCCTATTGATTTTGGCAGAGCACATCTGATTGAGTGGGA
 GCTTGTGCACTTGTCTTCACAGGAACACAGTCACTTTGCAACTATACTAGGCTTTTCTTGCTTTTGGAAAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAATTACTGAACATATTGTCAAATGGACTTCCTGTGATTT
 GTTGGCCATTACGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTTAAAGGATTTTCT
 CTTTGGAAAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTGTGGTGTCTCTGCTGAATTTAAATAT
 TTTATGTGTTTTCTGTTAGGTTGATTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAAAATATT
 TAGCTCCATTTATACAAAAATTTAAAAATTAAGTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTAAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGGAGTAAGGTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATCCAGTTTTTGAATCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTCTATGTTTTACCTGTAAAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAAATACACTTAGAAGTGTTTACTTACCTGGAATAATTTGCTATGCCGTACATT
 CAGAGTGCCCTCCCTCGCAAGGCCCTGCCATGATTACAAAGTAACTGTTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTAAAGATTTAGACCATGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTAAAGCAAGTTTCTGTATACCTCTGAAGTGTGTTTTGATTTTGAAGTTCATGATAGATCTGCTGTTT
 CCTTATAAAGGCATTTTGTGTGTGAGTTAATGCAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAACAAT
 ACCTGACCAAAAAATCCAGTAACAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTTATCAGGA
 CTTTTTTCAGGAGTGGGTTATAAAACATTCAGTTGGTCTGACAGTATTTTGTAAAGATATATTGTTGTATG
 TTTTATCAGTATACTTACATAAAAAATTTTCGCCATCAGCCAAACTCAGTAATCATGACAGCTGCTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTCACTTTTACTAAAGATGCCATAA
 AGCCACAGCTTTTATTGCTTAACCTTAAGCCATGACTTTAGATATGAGATGACGGGAAGCAGGACCAATATCG
 CGGTGCGGCTGGAGCCCTCCCACTGGAGGCTGAAAGTGGCTTGTGCTATTATATGTTTCAGATTTCAAGAGGA
 GGTGAGGTTACAGTGAAGTTAGAGAGCTGGTGAAGCTTGGGAACCTTTGTGCTTGTGATCTCAGTGCACTGACCTT
 TTTTTCAGAGGAGTGATCTCTCTGGTCTTCCCTATTTTCTGTTCTGGATCTCAGTGCACTGCACTGCTACTG
 TTTTATCAGTTGGCCACAGACTTTTCAACAGTCTGCTATTTCTATATACTAATTTGATTTGGCAGCATTT
 CTGCTCTTGACCTTGTATACTAGCTTGACATAGTCTCTCTCTGTTTCTAGGCTAGTTACTTGAGATATGAAT
 TTCCATAGAATATGCACTGATACACATATCCATTCTCTTATGGAAGAAAACCTTTTGTATGATGAACATAA
 AGATTTTAAATATCTATTTTAAAAA

[illegible]

MDFFLLGLCLYWLRLRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTEAPH
NLSGLGLSLRYNSLSELRAQQTGLMQLTWLYLDHNHICSVQGDAPQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRILTYIEPRIINSWSKSLTSIT
LAGNLWDCCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPSTG
HLLSAVTNRSLDGLPPASSATTLADGGEGQHDGTFEPAVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIIVLVLYVSCWCFPSLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYVVDYKPNH
IEGALVINNEYGSTCHOOAPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGCTTGAGTTCGCCGGCGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGGCTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTTGGCGTCCCGCGGGGCCGCTACGCTTCCACGGGCCGGCGCGCTGAGCGGTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCTGCTCCAGCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVS DMLLP LDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRS GDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLPGASPVRVRSISALGRFTTRDEDLAVFLASR
AGR LRFHGP GALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT
CTGCCITTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGC
CGTGTGCTCTGCATTAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
CTGGTGGACAGTTTTGTAACCTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTTCGAACATTGAGGGTTACTTTGGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAA

0503720144000

COPY

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCGGGGGCGTTCCCTCCAGTCACCCCTCCGCGCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATAGGGGGGAGAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTCTCCTCATACTTGCCTGCATGAGTCTTTC
 AACCACCTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTCTTTTGGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAAAGCCCTATTTTCATTATATATGAAATATGGTGTTCACGTGAACCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCTAACCATTTACTTTGGTAACTGGCGCTCTTTCGACAGAAATCATGGGATTGTC
 AAATGATATGTTTGGATCCTATTTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTT
 GGGAGAAGCGACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTCAGCCATGTGGCCCGGA
 ACAGATGTAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATGTTGAATGTTTACGTCAAAAGAGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCGCTGTCAATTCAGATATTGACAAAGAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCGAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCACTACCTGGATAAAGACCCTATACCCGTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGCTATGAAGCACTAATCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAGGTGGCATTACAAATACACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAAATATTTTAGCCCATGGTCTGCTTCAGAAAAGATTTTC
 TCAAAAGAGCCATGAAGTCCACAGATTTGTACCCACTACTATGCCCACTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAT
 CTATACTCCTCCCTGGTAGTGTTAAACAGCAGAAATATGACCAAGAGGGGTCTACCCCTATTTTCATAGGGGT
 TCTCTTGGCAGCATTATAGTGATTGATTTTTTGTAAATTTTCATTAAGCATTTAATTCACAGTCAAAATCCTGC
 CTTACAGATATGCTGCTGAAATAGCTCAACCATTTATACAAGCCTAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTCGAGATTCCATAATTTATGCTAGTGTTTAAAGGTTTCAAAATTCGGGAAACGATTCCAAACATCTGC
 AGAAACCATTAAGCAATTACATATTTAGTGATACACACACACACACACATACACACACACGGACCAA
 ATACTACACTGCAGAAAGATAAAGATGTGAGAGTATGTCCTCATTTTCACTGTAGCATAGGATAGATAAG
 ATCCTGCTTTATTTGGACTTGGCCAGATAATGTATATTTAGCACTTTGCACTATGTAAGTACCTTTATAT
 ATTGCACTTTAAATTTCTCTCCTGATGGCTACTTTAATTTGAATGCACTTTATGGACAGTTATGCTCTTATAAC
 TTGATTGAAAATGACAACTTTTGCACCCATGTACAGAACTCTGTTACGCATTTGTCAAACCTGAAGGAAAT
 TCTAATAATCCGAAATAAGACATAGAAATCTATCTCCATAAATGAGAGAAGCAAGAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATCTATTCCCAACAGCAGAAATGCACTGTGGCAT
 TTCTTGCTCTATTTCTTTCAGAGACGTTGGTTTCATTATTTTTCCTCAAAAGAGATCAAACTACTGACAG
 ATTGCTTCAAAATATATTTCTGTCATAAAATTTATGATTTCCTGATGATCATATTAAGTGTATTTC
 TAATAATGAAGACACCATGAATATACTTTCTCTATATAGTTCAGCAATGGCTGAAATAGAACCAACAGCA
 CCATCTCAGCAATGTTTCTCTTGTGTTGAATTTTTCCTCTTGGAAATTAATCACTATTAAATACATTA
 AAATCAAAATGGATAAAAAAGAAAAA

699721.1190

FIGURE 202

MTSKFILVSFILAALSLSSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDKHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG
 GACAGGCCACCTCGGGGCGGAGGCAGCCGGGTGAGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCTTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGAC**ATG**GCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC
 AAGGTGGCTCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTTCATCCTGGACATTGTCTCCTGTTCCAGAGCACCAAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGTGGCCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGAC**TGA**TGAGTTTGTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCGGCCAACAT
 GCTCTGTCTGTGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCCAGGTTCACAGTACTTTG
 AGTCGAAGGGGGCTCCCTGCCCAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCTCACCTTACCGCCAGTGGAGGCAGAAAATTGTACAACTGGAGATAAGGACCT
 TGATGGGCGAGCTAGACTTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTTTTAAATTTTGGACAAAAAAGAAATGATGGACGCATTGACGCGCAGGAGATCATG
 CAGTCCCTTCGGGGACTTTGGGAGTCAAGATATCTGAACAGCAGGCGAGAAAAAATTTCTCAAGAG
 CATGGATAAAAAACGGCAGCATGACCATCGACTGGAAACGAGTGGAGAGACTACCACTCCCTCC
 ACCCGTGGAAAAACATCCCAGAGATCATCTCTACTGGAAGCATTCACAGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCGAGACGGGGATGTGGTG
 GAGACACCTTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATCGAGTCCATGCCCTCCCGCAGCAACAACATGGGCATCGTTGGT
 GGCTTCACTCAGATGATTGAGAAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTCAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGACTCTGAGGATTCACAGAGAGGCTTGTGGCAGGTTCCCTGGCA
 GGGCCATCGCCAGAGCAGCATACCCAAATGGAGGTCTGAAGACCCCGATGGCGCTGGC
 GAGACAGGCCCTAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCTTGGCCAGAGAGGGGG
 TGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCTATGCGGGGATC
 GACCTTGCAGTCTCAGAGACTCTCAAGAAATGCTGGCTGCAGCAGCTATGTCAGTGAACAGGCC
 GGACCCCGCGGTCTTTTGGCTCTGGCCTGTGGCAGCTATGTCAGTACTGTCAGGAGCTGG
 CCAGTACCTCTGGCCCTAGTCTGAGCCCGGATGCGAGCGCAAGCCTCTATTGAGGGGCGCT
 CCGGAGGTGACCATGACAGCCTCTTCAAACATATCTCGGAGCCAGGGGGGCTCTCGGGCT
 GTACAGGGGCTTGGCCCCCACTTCATGAAGTCACTCCAGCTGTGAGCATCAGTACGTGG
 TCTACGAGAACCTCAAGATCACCTTGGGCGTGCAGTTCGCGGTGACGGGGGAGGGCGCGCG
 GCATGGACTCGCTGATCTGGGCGCAGCCCTGGGGTGTGCAGCCATCTCATTTCTGTGAATG
 TGGCAACTAGCTCTCTCGAGCCAAAGCTGTGAAAACCTAGACGCACCCGAGGAGAGGT
 GGGGAGAGCTGCGAGGCCGAGGGCTTGTCTGCTGACCCAGCAGACCCCTCTGTGGTTCC
 AGCGAAGACCACAGGCATTCCTTAGGTTCCAGGGTCAGCAGGCTCCGGGCTACATGTGTAA
 GACAGGACATTTTCTGCACTGCCCTGCCAATAGTGAGCTTGGAGCCTGGAGGGCCGGCTTAGT
 TCTTCCATTTTACCCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCCCTCTGGTCTGCCGTGC
 ATCTCCCTGTGGCCTCTTGTGCTGCTGCTGCTGCTGAGGTAAAGGTGGGAGGAGGGCTACAG
 CCCACATCCCAACCCCTCTGCTCAATCCATACCATGATGAAAGGTGAGGTCAAGTGGGCT
 CCCAGGCTGACTTCCAAGCTACAGCATTAACGCACACTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCTTGTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTGGGCTATCT
 TGGAGTGCAGGGGGCTCGGCGCTGCCTGGCTGCAACAGAGCAAGTCTGCGGCTCA
 TGGTGCTCTGAGCTGGCCTGGACCTGTCAAGATGGGCCCCACCTCAGAACCAAACCTCACTG
 TCCCCACTGTGGCATGAGGCACTGGAGCACCATGTTGAGGGCGAAGGGCAGAGCTTTGT
 GTGTTCTGGGAGGGGAAGGAAAAGGTGTTGAGGCGCTTAATTTAGATGTTTGGGAAAAGGG
 TTTTGTCCAGAAAGTAACTTTTGGGACTGGAGGCAGAAAAGGCCGCAAGGACAGGCGCTG
 CAGCAGGAGCTTGGCTGACCTGCTCAGAGTCTGCTTCAAGCCCTTGGGGCTTCTGTCTCAAC
 CGAGCAGGGGGCAGGGGACAGGCCACCCCACTTCCATCTGTGTGATCACTGCTTGAACCTATTT
 ATTTTGTATTTTATTTGAACAGAGTTATGCTCTAATATTTTATAGATTTGTTTAAATTAATA
 GCTGTGCTATTTTCAAGTTCATTTTATTCATATTTATGTTAGTTGTTTGTACCTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAGAGGGGGGCTTGGGCGCTGCAGTCACT
 CTGTTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGGCCGCAAGGACAGGCGCTG
 GCTCCTTCTCTTGGCAGGTGTGGGGAAGGGCTTGGCCAGCCTTAGGATTTTCAGGGTTTGA
 CTGGGGGCTGGAGAGAGAGGAGGAACTCAATAACCTTGAAGTGGAAATCCAGTATTTCT
 CTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTGCAAGGAGCTGAGGTGCCCTCT
 CACTGTGAATTTGTGTGGCGGGGGCTGGAGGAGGGGTGGAGGCTGGCTCCGTCCCTCC
 CAGCCTTCTGCTGCCCTTGTCTTAACAAATGCCGGCCAACTGGGCAAGCTCAGGTTGCACCTT
 ATTTCCACGATGACCTGATGAGGAAATCTCAATAGGATGCAAGATCAATGCAAAAATTT
 GTTATATGATGAACATAAATCGAGTCTGCAAAAAGCAAAATTAAGAAGAATTTGACGCTTAG
 AAGTTGTCTATTTAAAGCAGCTTCTAATAAAGTTGTTTCAAGCTGAAAAAAGAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFI PSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQA EKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNIGI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVLRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACCTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCGTATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTCTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAAGTGTGTTAAGAGTGATAAG
 TAAATATGCACGTGGAGACAAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAAATTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCTTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

[illegible]

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGLLYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

210/330

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCAATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTTCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGCTAAGAGTCTCGTGCTGAAAGGCTGTT
 CAACGTCAGTAACGCCACCTGTGAGTTCTGTCTGGTGAACAAGACTCTTGGAGGAGTCA
 TCTTCGAAAGTTTGAAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGGTCTGGGGCTGCACTTTGCCAGCACCCTTCTGCTTCTCTG
 AGGTCCAGAGCACCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCAATTATTA
 AAGCACTGGTTCAATCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECP SHANTSCISSASSSSLET PVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGECSNTSDALDP LKNVSSNAE
CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGC SNVSNATCQFLSGENK
TLGGVIFRKFE CANVNSLTPT SAPTTSHNVGSKASLYLLALASLLLRGLLP

2014-09-23 14:00

FIGURE 213

GGCCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
 GGGGTTGGCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCCCGCCGCCG
 GCGGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGGGGGCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGCTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAAT**GGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLLNIGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSyrSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFsRSSAINEDGSSEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPtAMPSPEDLRLVlMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQlRTEHKPC
TYQQcPCNRLREECPLDTSLCTDTNCASQSTTSTRTTTTFFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNslSSVFTEMQPIDRNQR

FIGURE 215

CCCGGTGCACCCACGGTCCGGGGAGAAAG**ATG**CCGGCCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCA
 GCGCGCCTGGCGAGCGGCTCCACGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCAGAGACA
 GAATCTGCTTGGGGGGCTCTGAATCACTTCCGCTCCCGCCAGCCAACTCATAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTGTGGGCTCTACCTCCAGGAAGGTACAAAGTGGCT
 CAGTTCATGGCAAGTGGCCCTTCTCCGGTTCCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCTCTGTTCT
 CAATGGCTGGCCAGGCTGGTGTGCTCTGCGGCTACCGCACTTCGTGCCAGGCTCTCCCCCATGTACACACA
 CTTGTGTGGCTTGGCTGGTGTGCTTCAATGCATGGTTCGTGGTCCACAGTCTTCCACACAGGGGACACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCTCCACTGTCTATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CTGCGGGCTGCAGCACCCAGCTGTGGTCACTGCTTCCGGGCTCTCTGCTGCTCATGCTGACCGTGCACGCTCT
 CTTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGCTATTGGCTGGTCAACGTG
 GTGTGGTGGCTGGCTGGTGTGCTGTGAACAGCAGCGCGGCTGCCTACGTCGCGCAAGTGGTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGTCTTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGCTCTTTTTCAGCTTCTGGAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAGCTGGACT**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCTGCCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTCTCTTTTCACTTCTTGAACCTTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTCTAGGG
 AAGGCCTCCAGCATCTGGGACTCGAGAGTGGGACGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGAAGTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTTCTCCTCCACAGCCTCTCCTCCACATCCCAAGTGT
 CTTGCTGGTGGTCTGAAGCCCTCTGTCTACCTGGGAGACAGGGACACAGGCCTTAGGGATACAGGGGGTCCC
 CTTCTGTTTACCACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTAGGGAGCAGGTGCTGGGATGGGAAGGAGTTTCACTCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATATCCCTTTAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCCTGTGCTGCTGTGCTGGTGGAGAGCTGCCACCCTGTGTGGGAGTGTGGGCCAGGCTGAGTGTATAGG
 TGACAGGCGCTGAGCATGGGCTGGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGAGAGCTGGGTTGTGT
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTCAGGGGGTGGTGTGTGTAGCGTGGGTAGGGGAGCTGTGT
 TCGCGTGTGCTGGTGGCATGTGAGATGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGAGCAGGAT
 GAGGAATCCTGTGACCATCAATATCACTTGTGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGC
 CAGGAGCTCTCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGTGGTCCCTTGTGCCGCTCTCTGCAAC
 CTCACAGGTCACCAACAAGTGGCTCCAGAGCAGCCCTCGGAGGCAGAGGAAGGAATGGGATGGC
 TGGGCTCTCTCATCTCTCTTTCTCCTTGCCTTGCATGGCTGGCTTCCCTCCAAAACCTCCATTCCCT
 GCTGCCACCCCTTTGCCATAGCTGATTTTGGGGAGGAGGAAGGGGCGATTGAGGGAGAGGGGAGAAAGCT
 TATGGCTGGTCTGCTTCTTCCCTTCCAGAGGCTTACTGTTCCAGGGTGGCCCCAGGGCAGGAGGGGCC
 ACATATGCTGTGGCTGGTAAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTCTGCCCAAGG
 AATAGAAATGGAGGAGCTCCAGAACTTTTCAATCCCAAAGGCAGTCTCCGTGGTGAAGCAGCTGGATTTTGT
 CTCCTGCCCTGAGCCCTTGTCCCTCTTTGAGGAGGGGAGCTATGCTAGGACTCAACCTCAGGGCTCGGGTG
 GCCTGCGCTAGCTTCTTTGATCTGAAAACCTTTAAGGTGGGAGGGTGGCAGGGATGTGCTTAATAAATCAA
 TTCCAGGCTCAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMFLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAFA
 VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC
CTTCCCGGGGTTCTGGGGTGACATTGCACCGCCGCCCTCGTGGGGTGCAGTGTGCCACCCCA
CGCGAGATCCCCAGCTGGCGCGCCCTCCCATTTGGCTGCTCGTGACAGGCCACCCCCC
TTCGCCACCTGACACGCC**ATG**GGGGCTGCGGTTCTTTTTCGGCTGCACTTTCGTGCGGTTCCGC
CCGGCCTTCCGCGCTTTTCTGTGACTGTGGCTGGGGACCCGCTTCGCGTTATCATPCTGGT
CGAGGGGACATTTTCTGGCTGCTTCCCTGCTCTGGCCCTGTGGCTCTGGTCACTGTG
TCCATTGTACAGCCAGCGCTCATAGTCCCGGCTCCAGTACGGCCCTCTGATTTTGGTGTCTGC
GTCTGTGCTCTTACAGGAGGTGTTCCGCTTTGGCTACTACAAGCTGCTTTAAGAGGCAGA
TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATACCCATTCCATCCGCGAGATGGCCT
ATGTTTCTGGTCTCTCTTCGGTATCATGATGGTGTCTTCTCTGTATCAATATTTTGGCT
GATGCATTGTGGCGCAGGTGTGGTGGGATCAGTGAGACTACCCCTATTACTCTCGACTTC
AGCCTTTCTGACAGCAGCCATTATCTGTCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
CCTGTGAGAGGAGCGGATCTGGGCTTTGGGGCTTGGTGGTGGGAGTCACTCATGACATGAC
GGACTGACATCTGTAACCCCTGGTATGAGGCGACCGTCTGCGCCATCTATGACGTACTGT
TTCCATGGGGCTCTGGGCCTTATCATCAGACTGGAGGGTCCCTCCGAAGTATTACGGCAGCC
TCTTGTGTAAGACT**TGA**CTACCTGACGCTGATCGCTGACAGTCCCACTGCCTGTCCACT
CCCATGACTGAGCCGACGCCAGCCCGGGTCCATTGCCACATTTCTGTCTCCTTCTGTGCT
GGTCTACCCCACTACCTCTCCAGGTTTGTGTTGTCTTTGTGACCGTTAGTCTCTAAGT
TACAGGAGCAGCCTGGGTTGAGCAGTCACTGAGTGTGGTTTGAATCTGCATCTATCCC
CACCACCTGGGGACCCCTTGTGTGTTCCAGGACTCCCCCTGTGTGAGTGTCTGTGCTCTAC
CCTCGCCAAAGACTACCTCCCTCCCCCTGCGAGCCGACGCGGAGGACGATCGGGTGAT
GGGTATTCTGCCTCGCATCCCAACCGAGACTGAGGAAACCTAGGGGGAGCCCTGGGC
CTGGGTTGCCCTCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTCTCGGACAGTGCAG
GTTGCTCAAGAAAGGCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTATCCCTCAAGACTGGACATCTTGGTCTTTTCTC
AGGCTCGAGGGGGAGCAACCTTTTGGTGTGATGATAAATACCTAAATCGCTTTTCTTTCT
GAGTGGGGGGAGGAGGAGGTATATGTGAACTCTTCAACCTCTTGGGTATATTTTCT
TCTCTCGATGTGCTCTCATGTGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCGACCT
GGGGGAAAGGAAGGAGTGCATGTTTGGGAAGTGGCATCTGAGGAATCAATGGTTTAACTC
CCTTAACCAACGAGCATCCCTCTCTTCCCAAGGTGAAGTGAGGGTGTGCTGGTGAAGTGC
CACTTCCAGAGCTGAGTGCACCTGAGGAGTCAAGTACGATGACATCGTAGGGAAGGAGG
GAGATTTTTTGTAGTTTAAATTTGGGTTGTGGAGGCCGGGAGGTTTCTATAAACTGT
ATCATTTTCTGTCTGAGGGTGGAGTGTCCCATCTTTAATCAAGGTGATGTGATTTTGACT
AATAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAA

220/330

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIILVAGAFFWLVSLLLASVWVFILVHVTDR
SDARLQYGLLI FGAAVSVLLQEVRFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVG IHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

0000722 11000

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

0998722:14:502

FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAATTCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

000722.14903

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCCACTG
ACCAGCCATGGGGGTGCGGTGTTTTTCGGCTGCACCTTCGTGCGTTTCGGCCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTTCGTCGCGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTGTGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTTGGTGTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAATGAACAGAAGAATTGTCGCCACTAAAGATGTGAGACCCAT
 CAACGTCTCCTCTCATTTGCCCTCTGTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCCCTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTACG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAACTGTCCAGGGCGGGGGTGTGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

000072.1490

FIGURE 227

ATGTCGCAACGACCGGCGAAGAACCATGGCGCGCGCTGCCCAACTTGAGGACCGGCGCGCGA
CRAAGCCGACGCGGCGAGCTGCGCTACGTGCTGTGCACCGTGCTGCGCCCTGGCTGTGTC
TGCTGGCTGTAGCTGTGCTCGCGTGTCGCTGCTCTCTGAAACACGCCACCGCGCGGGACG
GCGCCCCCACTGTCTGCTCAGCTCTGGGCGCTGAGCGCCAAACAGCGCCGCTGCTCATGTGA
AAGGCGCGGACAGCTGCACACTCAGCTCAGCGCTGATGAGCGCGCTGCGCCGCTCACCAGCA
GCTTCGACAGCTTGAGAGCGCGGACGCTGAGCGCTGAGCGCGCTGACAGAGCACACGGCCG
CAGCCACGGCTGGTGCGGACACAGGAGCAGGAGCTGAGCGAGACGCTGAGCGCTGAGCGGCT
CCGGCTGCTGGCCGAGCGCTCAGAGCTGACAGCGAGGATGAGCGAGCTGAGCGGCTGAGCGG
GCACGCTGGGCGCAGGGCTCAGCGCCCTGACAGTGTAGGACGAGCGGCTACGAGCTACGCT
TCTGAGAGCCAGGGGCGACATGCTCACTTGCTGAACTCGTGAGCGAGCTACGCTGATCGCT
CAGGAGGAGCCGGGGGCTGGGCGCGCCCGCCAAACAGGCGCACTCAGAGAGAGCGGCTGCT
GGGGAACCCGCGCCGGGGCTGTGCATGCTGCTCCGGCCCGAGACTGTCTGGAGCTGCTCT
CTAAGCGGACAGCAGGACGAGCTGGGCTCTACTCTGTCTTTCCACCCCACTACCCGCGGCTCT
CCAGTGTACTGTGACATGCGACGGAAGCGGCGCGGCTGGACGCTGTCTACGCGCGGGAGG
ACGGCTCCGCTGAACTCTTCCGGGGCTGGAGCAGCGTACCGAGACGGCTTTCGAGGCTCACG
GGGAGACATCGCTAGGCTCAGAAGGATCCACGCGTGCACACACAGGCTGCCTCAGAGCT
GCACGTGGACGCTGAGGACTTTGAGAATGGACAGGCGCTATGCCGCTACGGGAGCTTCGGCG
TGGGCTTGTCTCCGTGGACCTGAGGAAGACGGGTACCAGCTTACCGTGGCTGACTAATTC
GGCATCTCAGGCGCACTCCCTCTGAGGACAGCGGCACTGAGGTTACACCAAGGACGCTGTA
CAGCGACCAATCAGAGAACAACCTGTGCGGCTCTTACCGCGGTGCGCTGGTGTTACCGCAAT
GCCACAGCTCCCACTCAATGGGCGAGTACTGCGCGGTGCGCAGCGCTCTATGCGCAGGCG
GTGAGTGTGTCCTCTGACCGGCTGGCATGCTACTCACTAAGTCTCTGAGATGAAGATCCG
CGCGCTCGGGGAGGACCGCTAGACTGGTGCAATTTGCTCTGGCCCTGCTGGTCTGCTGCTG
CCCATCCCGACCCCACTCACTCTTTCTGTAAGTTGTTCTCCACCACTGTGCTCTGGCGAG
CCACTCTCCAGTAGGAGGGGCGGGGCCATCCCTGCACAGAGCTCCTCGGGCGGGTAGGT
CACACATCGCCTTTGCGCGCTCCCAACCCCTCAGATTTGGACAGCTACTGATCTCTTGCTCT
TGCTGATGGGGGCTGGCGAACTTGACGCCAACCTACTGCTGCTGCCCACTGTGACTCCGG
TGCTGTTTGGCGTCCCTGGCCAGGATGTTGGAGTGTGCCCGAGGACCCCTCTGCCCTGCC
GGCCAAATACCGGCAATTATGGGACAGAGAGCGGGGCGAGACAGCCCTGGAGTCTCT
CTAGCAAGTCTGGGGGAATCTCAGGTTCTCTGAGGTAGGTTGAGGCGAGTATCTCCAG
CGCTCCCAATGCCAACCCCAACCGGCTTCCCTGGTGCGCCAGAGAACCACCTCTCCCCAA
GGGCTCAGCGCTGGCTGTGGGCTGGGTGGGCCCATCTTACAGGCGCTGAGGTACAGGATGGG
CACTGTGCTGCGAGGCGCTGGGCTGCGAGTCTCTTACTCGTCTGCTGCGCACTGCTCTCTG
TCTCAATAGAGGCTTCTTCCACCCCAAGCTCCCGGCGGTCTCTCTACCTGGGCGAGC
CGGGGCTGCATCCCAATCTCTCCACCCCAAGCTCCCGGCGGTCTCTCTACCTGGGCGAGC
GGACTGCTCAATGGGAAGCTCTTGCTTTTGGGCTGGGCGCTAGGCGAGGCTGGGATGAG
GCTTTCAACACCCACCAACCAATTTCCAGAGGCTCAGGGGCTCAGGGCTCAGGGCGAGG
GGCTTGGGGGTGATGACCCCTTCCCTGAGGCTGCTCATGAGGAGGCCACCTCTGCTGCC
ATTGACGCTGGCCCACTGGACCCAGGCGAGCGCGCGGCTGCTCAGTACGGCCAGATCTGCT
CCACTCACCGGCAATGGGTGCGGGGACCTGGGACAGGACAGGCTCAGGACAGGACAGGCA
CTTTCTGTTGATCTCCCAACACCCAGCAGCTGTCACTCCCACTGCTGCTGCTGACACA
TCTCAGAGTGTAGACCCGCGAGCTCCAGGACACGACGACCAAGGCGAGGCTGAGGAGGCT
TCTCAGCTGTCTGCTGCAGAGCGCTGGACCCGCGTGTGCTTACGTCAGGCGCAGATCAGG
CGGCTCTTCAAGGCTCCTGATGGGGGCTCGAAAGGGCTGGAGTACGCTTGGGAGGCT
CGGTAGCAGCTCTCTCTCGGCGAGGAGGGGAGGTGGCTTCTCTCAAAGGACACCCGATGGA
GGTGCTCAGGGGGTGTGGGTTCTCGGTTCTTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAA
AACAATAAATTTGACTTGGCCACATCTGGGGTGTGGTGGGAGAGGCGGTGACCTGGCTCT
TGTCCGAGTGCCACAGGATCATACATCGCGAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDEQEELDLADQLPRLARASELQTECMGLRKHGTLGQGLSALQSEQRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFVRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYRYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

0
0
10
0
2
0
0
14
14
14
0
0
0

FIGURE 229

CGAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGACATTAGGAATGCCTTTTAGTGCCCT
TGCTTCTGAAC TAGCTCACAGTAGCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT
CACC GCTGTAGGAATCCAGATGATGAGGCCAAGTACAGCAGCACAGGGGACATGCTGGATGATG
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
TTTGTGCTTGGTGCTGCTGATAGGGGTGGCAGCCCTGGGGCTTTTGTTTTTTCACTACTACC
AGCTCTCCAATACTGGTCAAGACACCATTCTCAAAATGGAGAAAGATTAGGAAATACGTCC
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
AACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
GACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAAGAAGA
CTCTGGAATTTGCCGCTGCTCAGAGCTACTCTAGTTTTTCTACTCTTATTGGACAGGGCTTT
TCCGCCCTGACAGCTGGCAAGGCTGTGCTGGATGGATGGAAACCCCTTTCACTTCTGAAGT
TTCATATTTATAATAGATGTCAACGAGCCCAAGAACAGAGACTGTGTGGCCATCCTCAATGG
GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGAA
TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGTACTAGTACAAAATGGGTTCTCGTG
TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCACTGTGCCTTCTTG
GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACTCCCTGTTTTCAT
GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAA
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTTGGCAGTCACTTCCAGATTGTACC
AGCAAATACACAAGGAATTCTTTTTGTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT
CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAGACTCTGATAATTG
TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
AATCAACGTCCTCCGATATTTCCCTCAGAGAGATTTTCAAGACCAAAAAAGTGAGCCTCTTCA
TCTGCACCTGTAAATGTTTCACTTCCATGATTTTCAAGTACCCATATTTATACCTTTTACG
GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAAA

MQAKYSSTRDMLDDDDGDTTMSLHSQASATTRHPEPRTEHRAPSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQKWGHGDNICYFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPLDSGKAWLMDGTFPTSELSFIIIDVTSRPRSDCAVILNGMIFSKD
CKELRCVCYERRAGMPKSPKSHLVPETLGGED

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

231/330 11/10/2011 14:00

FIGURE 232

GCGGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCGCGGGG
 CCGGAGCCCTCGGATTCGCGCCCCCTCCCGGGTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTCGCGCGGGGCGGGGACCGCGCTCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGCGCCCGCAGGGCCCGTGGCCGTGGGCGATCTCCCTGGGCTTACCCGTAGCCCT
 GCTCAGCGTCACTTGGGTGGAGGAGCGGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCGCGCGGCAACACCAACGCGCGCGCGCGGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCCGGCGAAGGCGCGGGGAGAATTGGAGCGCGCGCTCTTGCC
 CTACCACCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTAGGACCCGCTACATCAGCA
 CGGAGCTGGGCGATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCAGCTGCCCC
 ACGCTGGGCGTGGCCGTGAACCGCAGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCAGGGGGCGCGCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTCTCTCTGGTGCCTGACACCACTACACCGAGGCGCACGGCCCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCCTCCGCGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGCG
 GAGAGCCACCCCGCGCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCATGCTGT
 CTCAACAACCTCGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTGTCGCGCGCCCTGA
 CGAGTGGCTGGTGCCTGCTGCATTCTCGATGCCACCGGGGTGGGCTGCCTGGTGACCACGAGG
 GGGTGACATATAGCCATCTGGAGCTGAGCCCTGGGGAGGCCAGTGACAGGAGGGGACCCTCAT
 TTCCGAGTGCCTTACAGCCACCCCTGTGCGTGACCCCTGTGCACATGTACCCAGTGCACAA
 AGCTTTCGCCCGAGCTGAACTGGAACGCACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCAAGCATCTGGCCGTTGATGGGACCGGGCGAGCTGTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCGGATGGCTCACCCGCTGCCACTGCTGGGGGTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACACCCCGGCTTGG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGCGCCGGGTATGGA
 ATACAGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGCGCCCGGCCCTCACTC
 GCCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCGCTATGTCACT
 GAGGCGTCACTCTCACTGTGCTGCTGCTGCTAGCTGCGGCTGAGCGTGACCTGGCCCGCTGG
 CTTCTTGAGGCGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGACCT
 GTCAGGCGCCAGCTGGCAGAGCTGGAGCGCGTTCCTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGACCTTCACTGCTGCGCTCATGGATCTACTCTCCAAGAAGCAGCCGCG
 TGGACACACTGTTCCTGCTGGCCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTTGAAACCG
 TGCGCATGTGACCATCTCCGCTGCGAGGCTTCTTTCCCATGCATTCCAAGCTTTCCA
 CCCAGTGTGGCCCCACCACAAGGGCTGGGCCCCAGAGCTGGGCGTGACACTGGCCGCT
 TTGATCGTCAGGCGAGCCAGCGAGGCTGCTTCTACAACCTCCGACTAGTGGCAGCCCGTGGG
 CGCTGCGCGGAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCCGCGCTGCTGCAGCGCT
 ACCGGCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTACACCCGCTGCTCCAGAGG
 GTGCTTGAAGGCGCTCGGCTCCCGAACCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACCT**G**AGCCCCACCTGTCCCGTGGGCGTGGCATGGCCAGCACCCCACTT
 CTCCCCAAAAACAGAGCCACCTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCACTGGTGCCTCTCTGCTCTGTGGGTCCCTGGGCTCTGGAACAGCACTGGG
 GGAGCTGCCCCAGAGCCACCCACTTCTCATCCCCAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTGGGGCTGTGGCTTCCACGTATTTATCAGTACAGCTGCGCTGAGCGGACCCGCTG
 CTCTGGGCGCTGGGGCTGGGCTGTAGAAGATTGTTGGGGAAGGAGGAGCTGAGGAGGGG
 GCACTCTCCAACTTCTCCCTTTTGGACCTGCCGAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGFVAVGISLGFLLSLLSVTWEEPCGPGPPQPGDSELPRPGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVRTRYISTELGIRQRLVAVL
TSQTTLTPLTGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFTGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCNRNDIVSARPEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFPSALTAHPVRDPVHMYQLHKAFARAELEERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLIYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAIISGWQAFFPMHFQVAFHFGVAPPQGGPPELGRDTRGRFDRQAASEACFYNS
DYVAARGRLAAASEEELLESLDYELFLHFHSSHLVRAVEPALLQRYRAQTCSARLSEDL
YHRCLOSLVEGLSGRTOLAMLLFVEOEGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCGAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTT
 TTCCCCGCCCCCTGAGACCCTGCAGCACCATCTGT**CATG**CGGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGCAGCGGCACGCGAGGGCTCCCGGCCCGCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

0000722: 44700

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTTGGCGGCAGCGCGACGCGAGGGC
TCCGGGCGCGCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACACACGTGGCAAGAGGACCCAGAACCCAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCAC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TTGTAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CGGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTTACAGGCTCTTTCCAAAGCCTTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCTATTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACGTATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACACAGTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCTGTCAAGTTGATTTGATGCCTTC
 ATCAGGGGGCAGGGAAGAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCTCAGCGGA
 GCCCTGCCCTTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTATCCTAGGCAT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCGAGAGAATGAGGCCCGCCAGTGCCCTTCTCTGC
 ATGCCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCTTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGTGCCTG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCCTCAGCGCCCTGTGCCCCA
 GCATGGTAGCAGCCAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCAGTGCCTGCTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCAGAACCTTCCACATCGAGGAGCCCGCAGAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**G**ATT
 CTTGCCCTTTCTCAGCAGCTGCACTGCGCTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCTGGACAGGTGAGGGC
 CTACAGCTGTGTTGCCGCTACAGGAGCCACAGCAAAATGTGGCATTGTGAATTTGAATTA
 CTTAGAAATTCATTTCTCACCCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGCTACTGTGTAGTGG
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSSELQREGVSHY
RLFPKALGQLISKYSRLREHLHSFTQGFWRTYWGPPFLQAPSGAELVWVFQDVTVDVDSKW
ELSNVLSGIFCASLNFDISTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLPCSSKAGLSVLLKADRLPHTSYHSQAVHIRVPCRNARCTSISELQRTLVSVPDAFITG
QGKKDWSLFRMFRTLTPECPPLASESRVYVDITTYNQNETLEVHPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFHLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLEMLIQLPANS
VTKVISQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLPFVSD
GSNYFVRLYTEPLLVNLTPTDFSPMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRARGVVPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGCTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGAATGCTGGGTCCCTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGAATCCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

5' 3' 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 240

MGSSSFVLVMSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

009072.1450

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCTCGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACC CGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCTTTGGCTTCTGGCTGTCTTGGTCTTCTTTCTCGCTTGCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAAGGAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCAAGGGCAAGCGCAACCAAGCCAAAGACGCTCATTTCCCAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACTAAGGAGAAGAAACCTCAGGCCACCCCAACCCCTGCCCTTTCCAG
 AGCCCCACGACGACAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGGCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAATATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGAGCCGCTGGAACACTTTGCACCAAC
 CTTTGGCTTCTATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTTGCCAGCCTTCCCGCTGGGAGCCTCCGGTGCATCACTGT
 GCCGTGGTGGGCACCGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGATGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCAACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTACATAAACCATGACTCTCAAGCTGGA
 GAGAAAGCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACAGCGCTCCTTGGTC
 CCGGAACCTGCCAAAGCCAAAGAA**TGA**CCGGGGCCAGGGCTGCCATGGCTCTCTTGCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTCTTGAAGTCTTCTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTTTAATTAATGGGGTGATGGGTGGCCAAATACCACAATTCCTGTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGCTAGAAAGCCTTTCTAGGAGTTATCTGATTCTGAAGGGCTCTACTTGTCCCTTG
 TCTTTAAGCTATTTGACAACCTTACGTGTTGTAGAAAACCTGATAATATACAAATGATTGTT
 GTCATGGAAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRRTTIYAEPAENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQLRMLAPTGAIVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLELDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTRFPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTDRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFAREALHMDRYLLHPDFL
 RYMKNRFLRSKTLGSAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CG**ATG**CGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAAGTTTCTAAAAACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAG**TGA**CGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGGAAACGAACAATCTTTATACACATCCCCTCATGG
ACAAGAGATTATTTTTCGACAGACACTTCCATAAGTCTTTGAGTTTGTATGTTGTTGTTG
ACAGCTTGCAGATATATATTGCATAAATCAGTGTACTTGCAGCTGTTATCTGTCACTTATTT

244/330

FIGURE 244

MRGPGHPLLGLLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

0000722-11902

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGTACCTGT
 ACCGCCGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGACGCCAGTATACCCATACCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAAC TAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGCAAGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTGTCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
 TCCGTGACGAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFC CGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

246/330

FIGURE 247

GGGGGAGCTAGGCCGGCGGCACTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGGCCCCAGAA
 CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTCTGCCCTCAAAATGGTCCCTTGCAACCATG
 TCAATTTCTACTTTCCCTACGTTCTGGCTCTCTTAAGTGTGTCCACTCCTTCATGGTGTCCAGAG
 CACTGAAGCATCTCCAAAACGTACTGTATGGGACACCATTTCTTTGGAAATAAAATACGACTTC
 CTGACTACTCTATCCGACTTCATTATGATCTCTTGATCCATGCAAACTCTTACCACGCTGACCC
 TTCTGGGCAACACGAAASTAGAAATCACAGCCAGTCAGGCCACAGCACCATCATCTGTGCA
 TAGTCACCAACTCTGCAGATCTTAGGGCCACCCCTCAGGAAGGGGAGCTGGAGAGAGGCTATTCGG
 AAGAACCCTCGAGCTCTGGAACACCCCTCAGGAGCAAAATTCGACTGCTGGCTCCCGAG
 CCCCTCCTTTGTGGGCTCCCTACACAGTTGTCTATCCTATGCTGGCAATCTTTTCGGAGAC
 TTTCCAGGATTTTACAAAAGCACTACAGAACCAAGGAAGGGGAATCGAGGATACAGCAT
 CAACAATAATTTGAACCCACTCGACCTAGAATGGCTTTCCCTGCTTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGGCCATTCCTCAATATGCC
 ATTGCTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCAATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCTTCACTATTTCAGATTTTGAGTCTGTGAGCAAGATAAAC
 AAGATGGAGTCAAGTTTCTGTTATGCTGTGCCACAGAAATAAATCAAGCAGATTATGC
 ACTGGATGCTGGGCTGACTCTCTAGAAATTTATGAGGATTTTTCAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGCTGCTATTCCGACTTTTCAGTCTGGTGTATGGAAACTGGGGAA
 CTGACAACATATAGAGAATCTGCTCTGTTTGTGATCGAGAAAGTCTTCTGCATCAAGTAA
 GCTTGAGTGCACAGTCACTGTGGCCATGAATCGACCTACCCAGCTGGTTTGGGAACCTGGTCA
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGCAATTTGCCAAATTTATGGAGTTTGTG
 TCTGTCACTGTGACCCATCTGAACTGAAAGTTGGAGATTAATTTTGGCAAAATCTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTTCTCACACCTGTGCTACACTGTGGAAATCCCTG
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAGGAGGCTTGATTTCTCAATATG
 CTAAGGGAGTATCTTTAGCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAACGA
 TAGCTATAAAAAACAAAAACGAGGACCTGTGGATAGTATGCCAGTATTTGCCCTACAG
 ATGTTGTAAGGAGGATGGATGGCTTTTGCTCTAGAAGTCAACATTTCTCTTCATGCTCACAT
 TGGCATCAGGAAGGGTGGATGTGAAAACCATGATGAACATTTGGAACCTGAGCACTGAGAGGCTTGA
 AGGCTCTGACGGCGGCCGCACTGGGTACCTGTGGCATGAATGGCTATTACATTTGTGCAATGAG
 AGGAATCCAACATGCTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGTGGAAATGGATCAAAATTTAATGTGGCATGAATGGCTATTACATTTGTGCAATGAG
 AGGATGATGGATGGGACTCTTTGACTGGCTTTTAAAGGAACACACACAGCATCGACGAGT
 AATGATCGGGCAAGTCTCATTAACAAATGCATTTACGCTGTGAGCAATTTGGGAAGCTGTCCAT
 TGAAGAGGCCCTGGATTTATCCCTGTACTTGAAACATGAACAGTGAATTTGCCGCTGTTTC
 AAGGTTTGAATGAGCTGATTTCTATGATAGTTTAAAGTAAAGTAAAGAGATGATGAATGAAGT
 GAAACTCAATTCAGGCTTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGCTCAGTCTCAGAGCAAAATCTGCGGAGTGAACACTACTCTCTCGCTGTG
 TGCAACATATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTCAGAAAGTGGGAAGGAATCC
 AATGGAATTTGAGCTGTGCTGACGTGACCTTTGGCAGTGTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTTATAGTAAATATCAGTTTCTTGTCCAGTACTGAGAAAA
 GCCAAATTTGAATTTGCCCTCTGCAAGCAACCAAAATAGGAACCTCTCAATGGCTACTAGAT
 GAAAGCTTTAAGGAGATAAAATAAAACTCAGGAGTTTCCACAAATTTCTTACACTATTGG
 CAGGAAGCCAGTAGGATACCCACTGGCTGGCAATTTCTGAGGAAAAACTGGAACAACTTG
 TACAAAAAGTTTGAACCTTGCTCATCTTCCATAGCCACATGGTAAATGGGTACAACAAATCAA
 TTTCCCAACAAGACGCTGTGAAGAGGTAAAGGATTTCTCAGCTTTTGAAGAAAAATGG
 TTCTCAGCTCGTGTGTCTCAACAGACAATTGAACCAATTTGAAGAAACATCGTTGGATGG
 ATAAGATTTTGAATAAATCAGAGTGTGGCTGCAAAAGTGAAGAGTTGAACAGTGTGAAAA
 TTCTCCTCTTGCCCGTTCTGTTATCTCTAATACCAACATTTGTTGAGTGTATTTTCAA
 ACTAGAGATGCTGTTTGGCTCCAAGTGGAGATTTTCCCTTCAACTCATTTTGTGA
 CTATCCCTGTGAAAGAATAGCTGTGATGTTTTCATGAATGGCTTTCTCATGAATGGGCTA
 TCCTACCATGTGTTTGTGTTCTATCACAGGTGTGCGCTGCAACGTAAACCAAGTGTGTTGGT
 TCCTGCCACAGAAGAAATAAGTACCTTATTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFFWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETHGFKYKSTYRTKEGELRILASTQFEPTA
 ARMAFFPCFDEPAFKASFSSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FTISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGD
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGHTTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMEKRDMMNEVETQFKAFLIRLLRLDIDKQTTWTDGSGVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKEKLQWLLDESFGDKIKTQEFQIILTILGRNPVGYPPLAQWFLRKNWNKLQKFELGS
 SSIAHVMVGTNTQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCTAGTAGCGCGGTATTACTGCTGCCCTCCTGGGGTTCATCTCCAC
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCAGATGGGCCCGGGCCTCTCCTGTATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGGA
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CAGGCCAGGTGCAACCTGCTCAATGGGACACAGGAATTGGGCCCTTGGGTATGACTGAGA
ACTGCAATAGGAAGATTTTCTGACCTGTCTCGGGGACACCATTATGACACAGGAAAC
TTGGCTCAAGAAACCACTGATTGGACACATCGAATACCAGATGTGCGAGGTGGGGCGAGGT
GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGTGTGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCTCCACTCAGCCCCCTCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCTTGGAACTGTTCAAGTGCTCCCCCGAATGACCTGCCCCAGG
GGCGCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGTCTCTTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGTTTGCCCTTCTCTGCTAACTCTATTACCCCCAGATTCTTACCCTGCTGTA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCCTTTC
CATTTCTGTCCATGAATCATCTTCCCCACACACATCATTCATATCTACTCACTTAACAGCA
ACACTGGGAGAGGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCCTGCTCTTCA

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRTVEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGLRCPVCLSMEGCLEGTTEECPKGTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTMECEVQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVPLGTCSSGSPRMTCPRGATHCYDGYIHLSSGGGLSTKMSIQGC
VAPQSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWGWVVC
PSC

GCGACGGGCAGGACGCCCGTTCCGCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGCGCT
CAGGATGAGGGGGAATCTGGCCCTGGTGGCGCTTCTAATCAGCCTGGCCTTCTGTCTACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGACGGCCTGGAAGAGTCG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAAGTGTGGGTCTGTAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCTTAATGGAGAACCAGGCGCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACACACAGGCTCTCTCAGCTGACCCAGCGAGCTCAAGTTCAATCAAGATGCTGTCGCC
GGTGTGCGCGACAGCGAGGAGAGTCTACTCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCACAGCTGTCTGCCAGGCGCGCGGGGCGACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGCGCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGCGCGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTTAGAGGAAAAATG
AAATGTTCTCTGGGGTGCTGCTCTGTGAAGAGCAGAGTTTCAATACCTGTGTTGTAGCCCCA
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAAACTTTTAAGTAGTCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

252/330

FIGURE 253

AGTGACTGCAGCCTTCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGACGAGGACACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCAATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGACGACAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCCTTAGTGAGGGTTTCTCGGCCC
CTTCATCCCAATCAGCTTGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTTTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCGAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCAGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAACCTGCA
TAGTGAATATCCCCAACCCCAATGGCTACTGAGTAGAATACCCCTAGAGTTCCTGTAGTGT
CCTACATATAAAAATAATGTCTCTATTTCTTCAACAATAAAGGATTTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNLGSGTK
SSLGTEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

GGGCGTCTCCGGCTGCTCCTATTAGACTGTCTGCTGCTGTGCCCGCTGTGCCTGCTGTGCC
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCTGGTGGTGTATCCCCCTTGGGGC
TGCTGTTCTCTGGTCTGCGGATCCCAGGCTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
CTGCTCAGCAAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGTCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCGGCTCCCGCCCGAGAGGCTGGCACCGGGGGTGGGGC
CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCATGCCCTG
AAACCTTAGACTCCCGGGGTAAACGATCCTGCTTACGCTCCCAAGTAGCTGAACTACAG
GCATGCACCATAGTGTGCCAGCTAGATTTTAAATATTTTGGAGATGGGGTCTTGCTCAAGT
TGCCACAGGCTGGTCTTGAAGCTCTAGGCTCAAGCAATCTCTGCTCAGCTCTCAAAAGTG
CTAGGATTATAGCAGTAGTCACTCCTGTCTGGCTTGCTGCTCTGTTCTTAACATCTGCCAAA
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTCCACTTGAGAGTCTCTCTCGCGTGGTTGCCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAACC GGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGT
GATTGTGATGGGTGTTCCAGGTGTGGTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
TGGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGACCACAGTCTTCCAGG
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
TTTAAACAAACCCAGTCCCAGCCTGGGTAAATGGTAAAGCCCCGTCTCTACAAAAAATC
CAAGTTAGCCGGGCATGGGTGTGCGCACCTGATGCCAGCTGCAGTGGGAGCTGAGGTGGAG
GTGAGGTTGGGGTGGGAGCTGAGGAAGGAGGATCGTTGAGCTGGGAGCTGAGGCTGC
AGTGAGCTGAGATTGCACACTGCATCCAGGCTGGGTGACAGAGCAAGACCCGTGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCTTGTCTCTCTTGAACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCTCTCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATTGCAAGATCTCAACCATGTGTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGCTCTTCTTGCGCCGGGCTTTGTCGCGGGGCTGACGAGGCGAGGCCAGCCACTTGTCTTT
CAGCAGGCCCCCCACCTTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

258/330

FIGURE 258

MGSGPLVLVLLTLLGSSHGTGPGMTLQKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS
VTLHHARSQHHVVCNT

090872Z 141900Z

FIGURE 259

AAATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAAGCTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATCTGTTTCTGATGTGGGGTCTCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCTCC
CTCCGATTGTTCTAAAT**TAA**TGTGAAAGATGTCTGCTGTGGAAGGCATGATTTAAATCTG
TATGATTCCTCAACCATCTTTAGTTGGGAAGGTCCTTGAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTGTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGGGCTATCAATATTTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAAGACTACTTGTGTGTAATAGCCTTTGAAATTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTGATTTCAAATAAACCAATTATGTTTGTAAATGATTAATAAAACCGA
ATAAAGTTCATATCTACCC

[illegible]

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTT
GAGAGAGGCCACGCATTAAGAGCATCGCCCTGCTTGGTGCTTTTGCAGGATGATGGTGGCCCTT
CGAGGAGCTTCTGCATTGCTGTGTTCTGCTTCTGACGTTTTCTGCCCCGCCGCGAGCTGATC
CCAGGACCCAGCCATGTGTGCATCATCTACACGCGCTTTCAGCTTCTGGAGCAGAGGGCTGG
AAAAATTGATCCCAAGCAGCAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAATAATA
TCTGTCATGCTGGGAAGATGTCAAGCATACACAAGTAGTACAGAAGTAGTGCAGTGGGTAACCT
GGCATCGAGAGTTGAACGCTGCCAACCGGGAGATTGACTACATACATACCTTCGAGAGGCT
ACAGGTGCATCGTATCAGAGGACAAGACATGGCAGAAATGTTGCTCCAAGAAAGCTGAAGAA
GAGAAAGAAGATCCGGACTCTGCTGCACTGCAAGCTGTGACAACTGCTGATGGGCATAAAGTC
TTTTGAAAATTAGTGAAGAAGATGATGACACACATGGCTCTTGATGAAGAAGTGTCTGTATAT
ACTCTCCAAAGGTGTACTTATTAATTGGAATCCAGAAAACAACATGTTTGGGAATTTTGCAAA
ATACGGGCATTATCAGGAGATAACCAACGACGCTCCCCGGAAGCAAACTTCAACAACTTTC
CTGGCAGGGAACAGGCCAAGTGTATCAACAAAGGTTTCTATTTTTTCATAACCAAGCAACT
CTAATGAGATAATCAAAATGAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
GGAGGGTTAGGCCGAGCATTTGGTTTACCAGCATCCCCCTCAACTTACATGTACCTGGCTGT
GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCACCATAGCCATTTGGTGTCTCA
CAAGAATTGAGCGCGGCACATCGGAAGTGAGCACTTATCGGATACCCCATGCGAAGAGCCAG
GATGCTGAAGCCCTCATTTCTCTTGTGTGGGTTCTCTATGTGTGTCTACAGTATGGGGGGCA
GGGCCCTCATCGCATCACTGCATCTATGATTCACCTGGGCATATCAGTGAGGAGCACTTGC
CCAACCTGTTCTTCCCAAGAGACCAAGAAGTCACTCCATGATCCATTCAACACCCAGAGA
AAGCAGCTCTATGCCCTGGAATGAAGGAAACCGAGATCAATTACAACCTCCAGACAAGAGAA
GCTGCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCATGTGGCTTTGGCAGCTGTTT
TACAGGACAGTGAGGCTATAGCCCTTCAACATATAGTATCCCTCTAATCACACAGGAAG
AGTGTTGAGAAGTGGAAATACGTATGCTCTTTTCCAAATGTCACTGTTAGGTATAGTTCTTC
CAAGAGCTTAGATGAGGACATATCATCAGAAAGTTTCAACATCTGCTTACTTCCCCAAA
CCTCTGGCTCTCAAGGATGACCACATTCTGATCAGCCTCACTGAAGCCCTTTTGTGTTTACT
GCTCCCCAGCATTTACTGTAACTCTGCCATTTCTCCCTCCCAACATTAGAGTTGTATGCCAGC
CCCTAATATTCCACCCTGGCTTTTCTCTCCCTGGCTTTGCTGAAGCTCTTCCCCTTTT
CAAAATGCTATTGATATTCTCCCATTTCTACTGCCCACTAAAATACATTAAATATTCTTT
CTTTTCTTTTCTTTTATTTGAGACAAGGCTCACTATTGTGCCAGGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCTCTCGCTCCAGCCCTCAATAGTACTGGGATTACAGCATGTGCAC
CACACTGGCTTAAAAATCATTTTCTTATTGAGGTTTAACTCTATTTCCTTAGCCCTGTCT
CTTCCACTAAGCTTGGTATGATTAATAATAAAGTGAATAATAAACATTGAATATGCTGTT
CCAGGTGTGGAGTGTTCGACATCAITGAATTTCTGTTTCACTTTTGTGAACACTGCACAG
TCTTTTACAGCTGTCACTTCAAGTTTTAGTGAGTAACACATAACAAGTGAAGATACAGC
TAGAAAAATACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
TGTTCACTTACTCTTATGATCAGATCGGCTCACTGTTTCAAGCTTAAAAATATAGTCTGCC
TTTAGCCAGTTTTCATGCTGCACAGAAGCTTTCAATAGGCCCTTCAAGATGATAATCTCTCC
AGAAAACCCAGTCAATAGGCTGAGGACCCCAACTCTAGCCCTGCTTGTCTGTCTGCTCTGTT
TTCTCTTTTCTGCTTTTAAATTCAAATAAGATGACACTGAGCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNASCNDNMLMGIKSLKIVKKMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILLTSLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPSSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330

FIGURE 264

MELSQMSELMGLSVLLGLLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWS TKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTGTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGTA
 AATGGCAGAAAGGACATTCCTCCCTCCCTCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCCTCTCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCAGGTCCTGGCCTGACCTCAGGCCCTTCAGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCTCTCCCTCGATTGGTTAACTCCTTAGTTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CTTGTGACCTTCTGCCAGAATTGTGATGCCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCACACAGCTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG
 CAACTACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEETCHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

266/330

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAGGCGCGCAGAGGGAGGCACCTTGAGAAATGTCCTTTC
 CTCACGAGACCCAAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAAGTGAAGGATTTCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGCTCGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTCTGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGACCGAGAAAAAGATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCACTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTELEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

0000720141900

FIGURE 269

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCCATGGCGAAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTCCTTCATCCACGACTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCGGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

270/330

FIGURE 270

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLEKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

0000700.141000

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTCTGTCTACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCCTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAATCAGTAACTGATTTTACTCTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCCTGCTGCCACAGTCAAATACTTCCTTCATTAAAGCTGAATAATATGGCTTTGAAGATA
 TTGTCAATGTTATAGATCTCTAGTGTGCCAGAAGATGAATAATTTGAACAAATGAGGAT
 ATGTGCTACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAA
 TGTATCTATATTAATTTCTGAGAAATTTGAAGGAAATCTCTAGTACAAAAGGCCAAAACATG
 AAAACCAATAAACCATGCTGATGTTTATAGTTGCCACCCTTACACTCCAGTACAGTGAACCA
 TACACCAAGCACTTCACGAAATTTGGAGAGAAAGCGCAATACATCTCACTCAACCTGACCT
 TCTACTTGGAAAAAAACAAATGAATATGGACCACAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTTCATGAGTACAATGAAGATCAGCCTTTCTACCTGCTTAAG
 TCAAAAAAATTCGAAGCAACAAGTGTTCGCAAGGTATCTCTGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGCGAGCTGCTTAGTACGCAATGCAATTCATCAACAAACTGTATG
 CAAAGATTTGTCAATCTTTCTCTATAAAGTACAAACAGAAAAAGCATTCATAAGTTTATG
 CAAAGTATTGATCTGTTGTTGAATTTTGTAAACGAAAAAACCATATCAGAAGCTCCAAG
 CTAAGTATTAATAAGTGAATTTTGAAGTACATGGGAGGTGATTAGCAATCTCGAGATT
 TTAATAACACCATACCCATGGTGACACCACTCTCCACCTGTCTTCATTGCTGAAGATC
 AGTCAAGAATTTGTGTCTTAGTTCTTGTAAAGTCTGGAAGCATGGGGGTAAGGACCGCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGAGAGTGTGAAATGGATCTGGG
 TGGGGATGGTTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTATCCAAATAAAAAGC
 AGTATGAATAAAGCAACACTATGGCAGGATTACCTACATATCTCTGGGAGGAACCTCCAT
 CTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATTTCCCAACTCGATGGAT
 CGCAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGATTGATGAAGT
 AAACAAGTGGGGCCATTGTTTATTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACGAGGAGGAAGTCATTTTATGTTTGCATGAAGTCAGAACAATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCGAGAGTCCCTT
 CAGCTCGAAAGTAAAGGATTAACACTGAATAGTAATGCTGGAATGACGACACTGCTATAAT
 TGATAGTACAGTGGAAAGGACACGTTCTTTCTCATACATGGAACAGTCTGCCTCCGATA
 TTTCTCTCTGGGATCCGAGTGGAAACAATAATGGAAAAATTTCAAGTGGATGCAACTTCCAA
 ATGGCCTTATCTCAGTATTTCCAGGAACCTGCAAGGTGGGCACTTGGGCATACAATCTTCAAGC
 CAAAGCGAACCAGGAAACATTAACTATTACAGTAACCTTCGAGCAGCAAACTCTTCTGTGC
 CTCCAATCAGAGTGAATGCTAAAAATGAATAAGGAGCTAAACAGTTTCCCCAGCCCAATGAT
 GTTTACGCAGAAATTTCTACAAGGATATGTACCTGTCTTGGAGCCAATGTACTGCTTTCAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAATTTACGGCTCCCACT
 GAATGAGCCCGGTACATACAGGCTGGGTAGTGAACGGGAAATTTGAAGCAAAACCGCCAA
 GACCTGAATTTGATGAGGATACCTCAGACCACCTTGGAGGATTTGAGCCGAACAGCATCCGGA
 GGTGCATTTGGGTATCACAAGTCCCAAGCCTTCCTTGCCTGCAAAATACCCACCAAGTCA
 AATCAGACACCTTGATGCCACAGTTCATGAGGATAAAGATTATCTTACATGGACAGCACCAG
 GAGATAATTTTGATGTTTGAAGAAAGTCAACCTTATATCATCAAGAATAGTGAAGTATTTCTT
 GATCTAAGAGCAGATTTGATGATGCTCTTCAAGTAAATACACTGATCTGTCAACCAAGGA
 GGCCCACTCCAAGGAAAGCTTTGCATTTAAACCAGAAATATCTCAGAAGAAATGGCAACCC
 ACATATTTATTTGCCATTAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT
 GCACAAGTAATTTGTTTATCCCTCAAGCAATCTGATGACATGATCCACAGCTACTCTC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTAGCTGGTAT
 TGTCTGTGATTGGGCTGTTGTAATTTGTTAACTTTATTTAAGTACCACCAATTTGAACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTTCAATCCCATGTGTGATCATAACTCATAAAAATTAAT
 TTAAGATTCGGAAGAGGATACCTTTGATTAATAAAAAACACTCATGGATATGTAAGGATGT
 CAAGATTAATAATTTAATGTTTCATTTATTTGTTATTTTATTTGAAGAAATAGTGAAGTAA
 AAAGATATCTTTTCTACTGATACCTGGTGTATATTTATTTAGTGAACAGTTTTCTGAAAT
 GATATTTCAAATTCATCAAGAAATTAATACTATCTAGTATGTCARAATCAAGCTAAG
 GGAGAGCAAAATAACAACATTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLVCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSGCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDfKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPIVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGYSKLVRAHG
 GANTARLKLRPFLNRAAYIPGWVNGEIEANFPRPEIDEDTQTTFLEDFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQAQVTLFIP
 QANPDDIDPTPTPTPTPTDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGACTAGCAGCAAAGACCGGGAAAGACCATTACGTCCTCCG
 GGCAGGGGTGACAAACAGGTCATCTTTTGTATCTCGTGTGGCTGCCCTTCTTATTTCAAGGAAAG
 ACGCCAAAGTAAATTTTGACCCAGGAGGCAATGATAGCCACCTCTCAACCTTCCCTTCTTTGAAC
 CCCAGTTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACAGCAAGCGGCTCCTTCGGCTTAACTT
 GTGGTTGGAGGACAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGTCTCAGAAGTGACTTGCCTGA
 GGGTGGACCAAGAAAGGAAAGGTCCCCTCTGTCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGTGAAGAACTTGAAGATTTCACTTCAGTCATTGCTTCTCGCTGCAAGATCACTCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAAGGAAATGGATG
 CAAGCAGCTCCGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTTCGGTGGG
 GCCCCGGCTTTGAGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGTAATGATGATGGTTCGCC
 GGGGGCTGCTTGGCTGGATTTCGCCGGTGGTGGTTTGTGGTGGTCTCCTCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCTCGACCCAAAAGGTGACGAGGAGAGGCTGGGCACTGCCAGGGGCCAACAGC
 CCCACGGGGAAAGAGGGGTACAGCGGCGTCTTCAGGAGTGGGAGGAGCAGACCGCAACTACGTGA
 GCGCTGTGAAGCGCAGATCGCACAGCTCAAGGAGGAGCTCGAGAGAGGAGTGAAGCAGCTCAGGAA
 TGGCGAGTACCAACCGCAGCATGCTCTGCTGGGTCTGGACAGGAGCCCCACAGAAAGCCAG
 CGCCAGCTCTGGCCTTCTCGACTCGCAGGTGGACAAGGCACAGCTGAATGCTGGCTCAAGCTGG
 CCACAGAGTATGACGAGTGCCTTTCGATAGCTTTACTCTACAAGAGTGTACCAAGCTGGAGACTGG
 CCTTACCCGCCACCCGAGGAGAAGCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGAGCCATT
 GAATCAGCCTTGGAGACCTTGAACAATCTGCAAGAAACAGCCCCAATCAGCGTCTTACACGGCCTT
 CTGATTTCTATGAAAGGATTCACCGAACAGAAAGGACAAGGGAATCTGTATGAGCTCACCTTCAA
 AGGGGACCAACAACAGCAATTCACACGGCTCATCTTATTTTCGACCATCAGGCCCATGAAAGTGA
 AAAAATGAAAAGCTCAACATGCCCAACAGCTTATCAATGTTATGCTGCCCTTACGAAAAAGGGTGG
 ACAAGTCTCCGGCAGTCTATGCAAGATTTTCAGGGAGATGTCATGTAGCAGGATGGGAGAGCTTCATCT
 CACTGTGTTTATTTTGGGAAAGAAATAAATGAAGTCAAGGAATCTTGAAGAACACTTCCAAA
 GCTCCCACTTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGAGCTTG
 ATSTTGGAGCCCTCTTGAAGGGGAAGCAACGTCTCTCTCTTTTCTGTGATGTGGACATCTACTT
 CACATCTGAATTCCTCAATCTGTAGGCTGAATCAGACAGGCAAGAGGATTTTATCCACTT
 TCTTCAGTCAGTACATCTCTGCCATAATATACGCCACCATGATCGAGCTCCCTCTTGAACAGC
 AGTGTGGTCTATAAAGAGAACTGGATTTTGGAGAGACTTTGATTTGGATGACGTCTCGATATCG
 GTCAGACTTCATCAATATAGGTGGGTTTGTATCTGGACATTCAAAGGCTGGGGCGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGAGCGCTGTGCGAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCAGGAGTACAAGATGTGCATGCAAGTCCAA
 GGGCATGAACGAGGCATCCACGCGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
 CTTTCGAAACAGAAACAGAGACAGTAGCAAAAAAATCAAGTCCAGAGAGGATTTGGGGAGA
 CACTTTTCTTTCTTCTTCTCAATTACTGAAAGTGGCTGCAACAGAGAAAAAGCTTCCATAAAGAGCG
 ACAAAAGAAATTGAGTGTGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTGGGCTTTTTAC
 AACAGAAATCAAAATCTCGCTTGTGCTGCAAAAGTAAACCCAGTTGACCCCTGTGAAGTGTCTGACA
 ACGCAGATGCTGTGAGCTTATAGCTTATAGTGTAAATGCTGGAGGTTTGTATGCTGTTTACAATACAT
 GAGACTGTTCTTTTGTGCTCATTGAATATCATGATTAAAGACATTTCTAAAAATTCAT
 TAGCATGAAAGGACAGCATATTTCTCTCATATGAATGAGCTATCAGCAGGCTCTAGTTTCTAGG
 AATGTCAAAATATCAGAAGGCGAGGAGGAGATAGGCTTATATGATACTAGTGAATACATTAAGTA
 AATAAATGGACCAAGAAAGAAAGAAACCATATCGTGTATTTTCCCAAGACTTTAACCA
 AAAATAATCTGCTTATCTTTTGGTGTGCTCTTTAACTGTCTCCGTTTCTTTCTTTTAAAAAT
 GCACCTTTTTTCCCTGTGGAGTTATAGCTGCTTATTTAAATACCACTTTCGCAAGCCTTACAAGAGA
 GCACAAGTGGCTCATATTTTATATTTTAAAGAGATCACTTGTAGATGCATATGAGAATCTGA
 GTCAAGAGCATCAATTTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGCGAGCAGTTCAT
 GTGAGGCTGTGAGACATAGGGAAGGAATGGTTGTACTAATAACAGACGTACAGATACCTTCTCTGAA
 GACTATTTTCAAGAGGAGCACTGAACACTGGAGGAAAGAAATGACACTTCTGCTTAAAGAGA
 AAGCAACTCATTCAGATCGGTATCTGTATGTACCTAAAGTCAAGATATCCGTGAACCAACATCTCT
 GAAGTAGGACCCCTTCTTACCTTTTAAATTAACAGTATCCGTGAACCAACATCTCT
 TTTCAAAACAGGCTGCTCTCTGCTGCTTCTGCTTCCATACAGCAAGTGAAGCAATATATAT
 ATATATATATTTGGAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAATTTTGTCTACAT
 GTTATCCACCTAGGAGGTGAAGTAACCTGAATTTTAAATTAAGCAATCTTCACTACATCA
 CCAAGATGCTTCTGAAATTTGCAATTTTATATACCATTTCAAACTATTTTAAAAATAAATACAGTTA
 ACATAGAGTGGTCTTCTTCACTATGTGAAATTTATAGCAGCACAGTCACTGAGCTAATATCT
 CTTTGAGTCTCTGCTTGTGTTGCTCAGAGTAACTCATTTGTTTAAAGCTTCAAGAACATTTCAAGC
 TTTGTGTGTGTTAAAAATGCATTTGTATTGATTGCTGCTGATTTTATGAAATTTAATTAACAC
 AGGCCATGAATGGAAGGTGGTATTCACAGCTAATAAAATATGATTTGTGGATATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKEFKRLILFRPFSPI
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLT VVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSKKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCCTCTTTCTAAATGACCAAAC
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATCTCTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAGCAATCAATTATACCCCAACACCCTGAAATCATAAGCTATTTCACGAC
 TCAAAATATTCTAAAAATTTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACTTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAA

AACCTCAAACCTCCTCTCTCTGGGAAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCCTGGCAGG
GTGTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGC GGTCCTTCTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTCTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGA
TGCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTCTGCTCTGGCCATTCGCTCTGCTCTGCTGTCACGATGATCAT
AATAGTAATTGTAGTGGTCTCTCTCCAGCATATCCGGAAAAAGCGATGGCGCGAAAGAGCTC
ATAAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA
GAACCTAGTATTTCTTGAAGTTAATGAAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACAGTCTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
GTGTAATTTTTCAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTGGCCCTTAA
GACACTACTACAGTGTTATGACTTGTAATACACATATATTGGTATCAAGGGGATAAAGCC
AATTTGTCTGTTACATTTCTTTACGTAATTTCTTTTAGCAGCACTCTGCTACTAAAGTTA
ATGTGTTTACTCTTTTCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAAACAGTAATCCTAAATCAAAGTGTAAATGACATTTTTATTTTTATGTCTC
TCCTTAACATAGACACATCTTGTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
TTTTCG

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCGTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGCTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCCTGTGATTTT
ATCCAACCTACTTACCTTGCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAAGACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

2025.11.14 09:20

FIGURE 285

GTCTATGCGCCAGTGCCTGCTCTGTGCGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCAGGAGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCGCACAAATAGAACTCCTGGGCGAGGAGTCA
CGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGTGAAGTGTCTGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTGTAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCGCTCAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CTGTGTTACTGGGATCAGCGAGGCGCGGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC
CAGGCGGGGACAAGGACAGGATGTAGCCCCATTGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCTGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAA

MPVPALCLLWALAMVTRPASAAPMGGPQLAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTEIELLGGQVSRGRDAAQLRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQRRLRQ
IQERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGAGGCTTGCCCCAGAGCCATGGCAAAGAAATGGACTTGTAAATTGCAT
CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCAAGAACTCCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
ACCGTGACAGCCTAACGGTGGAAGCGAGAAAAGTGTGTCTGTTCTCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCCTGTCGCAGCAGCAAGAGATACATATGCGAGTTACCATCCC
TAA**ATAG**GCTCTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTCTATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
TCTTGGGGTATAGGGGATCAGAAATATTGATCCTATGCAGCGAGATAAAATGGCTTCTGCT
AAACAGACTCAAAATCTTTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATCTCTGCCATGCTGGCAATAATACC
TTGTGAGCCCATACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTGTCT
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTCTTCATGCC
TACCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATTTGAT
CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
TGGAAGCTGAAAAGTGAATTTAAAGAATGCTATCTTGAAAAATTGCATACGTCGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAAAAGTTCATTGCT
TAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTGAAGCAACAATTTT
AAATATATTTTGTCTTCAAATAAATAGTGTTTTAAACATGATGTGTTTTGTGAACAATAT
CCCATTTCGAACTTTAACTACACATGCTTGAATTAGTTTTAGCTGTTTTCATGCTCA
ATAATTAAGGCTGAATTTCTGATCAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKFHEANEDCISKGILVIPRNSDEINALQ
DYGKRS LPGVNDFWLGINDMVTGKFPVDNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCCAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGCGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAAACCCCGCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

290/330

FIGURE 290

MKLAALLGLCVALSCSSAAAFVLVGSAPVAPFVAALESAAEAGAGTLANPLGTNLNPLKLLLS
SLGIPVNHLIEGSQKCVNELGPQAVGAVKALKALLGALTVFG

090720 141000

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGACGGCATCACATGAAGGTGGTGCCAAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGAGCCTGCTGCCAAAGATCTCCATTGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCACCAAG
 CCGGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCGCAACCTGGAAC
 GGGCCTCTCAGAGGGGAGTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCCATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAATTAAATCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCCGTGCTTCACCGAAGTCGACACTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGACGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGAGACA
 TGGCTCAGAAACATGAAACACAGAAACATGGAAGTTTCTTCCGAAGTTCAAAGTATAGTCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGATCTTCTCACCCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAAGAAATAC
 TGCTTATTCATGCCTCCTGTCTCAAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTGTCTTAACTAGTTTAGGTTGTTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATTAACAGTCAAACTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTCATCAGAATGGCATGC
 TGCTTAAGACTTTTAGATGTTTATTCTGGAATTTTTTCATTAAATGTTTTTGGACCATGGT
 TGACCATGGTTAAGTGAAGTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCTTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGAGCCTCCGAGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCAGAAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCTGGGCCGTGTCCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAGAAGACCAAGACCACA
TCTACCACCCCACTAGGGGCTCCAGGGGCCATCACTGCCCCGCCCCGTGCCAAGGCCCAGG
CTGTTGGGACTGGGACCTCCCTACCTTGCCCCAGCTAGACAATAAAACCCAGCAGGCAAA
AAAAA

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAPKVP IKMQVKHWPFSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQPKLLTTEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGFEEEDQDHIYHPQ

294/330

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGTGCAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGCACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
 TGTTTCAGTTACAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
 CCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCAAGGATGGAGAACAACCTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCI GGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
FYR

60
65
70
75
80
85
90
95
100
105
110
115
120
125
130
135
140
145
150
155
160
165
170
175
180
185
190
195
200
205
210
215
220
225
230
235
240
245
250
255
260
265
270
275
280
285
290
295
300
305
310
315
320
325
330

FIGURE 297

GCGGAGCCGGCGCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGTGGGAGCC
 CACGAGGCTGCCGATCTGCGCTCGGAACAATGGGA CTGCGCGCGCAGGTGCTTGGGCCG
 CGTGCTCTCTGGGACGCTGCAAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACT
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTGGTTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTAA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNITTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCGACCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCTGGCGCTTTCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCCAAGAAATTTGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAATATGAAGAAAGAAGCTCTGTGACAAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATCTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAGGTTGACTGAAAGAAACAGGCAGACAA
 CTGGAAGAACTGACTGGGTTTGTGCTGGGTTTCATTTTAATACCTTGTGATTTTACCAACT
 GTTGTCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTAAAGACACAGCTCAAAGTCAAGCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTAACTTGACTTTCAAGATAATTTTCAAGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTCAAGTCACTTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTG
 TCAGCATTTCGGTCTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGTTGTGGTGCCTCTTCTGAAAGGCTTAACCATTTTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTTTGAATGTAAACATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSCLALSLLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSVTKVTIIYLSILGLLL
LYMVYLT
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVE
YAQQRWKLQVQEQ
RKSVEFDRHVVL

000072-1100

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTTATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTACATAAGAATG
TTTACTCAATGTTTAAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTACGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG
AGCACAGAAGTAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTTCGCCAATGACGGTTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGTCTGCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGCTCTGGGCCACTCTACCAAGTGATTTTCAGACTCCCGCTCTC
CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCTCAAACCCCCGTT
GGATCAGACCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCA

FIGURE 305

CTATGAAGAAGCTTCCTGAAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACCTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGTCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTGACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 307

CCCACGGCTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGG
 CCCGGGGCTGTGGCGTCGATCCGACCCAGGCAGCCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCGGGAGAA
 GCCCGGGCAAACGCGAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTACGAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTAACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTATCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAAACAAACAGG
 CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKNKNLVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCC
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGTTGGGTTCCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTAA
 ACCACGCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCGAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCG
 CGCAGCGGCGCTGTGTCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGTCTCCTCATCCTG
 CTGTCCAAAGTGCAGTGTGCGGGGGGCGGCCCGCGCGCCGGACCGCGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACGTGTTCTGCCGCGCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTCACCCACTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCAACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTAAAGGAGTGTGTCT
 TTGAGAAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCTGTCTGCGCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIQKREVRPEGGSRPVSAQRVRCPRGTSKLCQKQLLILLSKVRLCGGRPAPDR
GPEPQLKGIVTKLFCRQGFIYLANPDGSIQGTPEDTSSFTFNLIPIVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENIYVLYASALYRQRSSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLSVPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACAT**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
 RQDPQLKGIVTRLRYCRQGYLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKFPVNKSKTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

000072-14000

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGAGCTTTCTCCTGGAAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AAATAAACCCAGAGTTAGACCCCGGGGGTTGGTGTGTTCTGACATAAAATAAATACTTTAAAGCAGCTGTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCAATT
 TTCTCTATAAAGGAGAAAGTGACCGAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAGATAA
 AGAAGCTGGTGGTGGTGTCTTTCTTTCTTTTGAATTTCCACAGAGGAGAGGAAATTAATAATACATCTGC
 AAGAAATTTAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATTCAGCGATAATTGACGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCCCTGGATTCCATCT
 GGATGTTGCTGTGATCAGCTGGAATACAACTGTTTGAATTCAGAAGGACCAACAGATAAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACAGCTTCAGCAAGGTGATTGTGTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAGTGAACAGCTTCAAGCATTGAG
 GCACCTTGGAAATCTCATACCTTGTAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAACTGCTTACTACCATCCGGAATGGAGCTTTGTATACCTTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAACAACCCATTGAAGAGCATCCCTCTTATGCTTTTAACAGAATTCCTCTTT
 GCGCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAAT
 T'GAGGTATTTGAACCTTGACATGTGAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTAICTGCCATCAGGCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTTGCATCATCTAGACGGATACAT
 TTACATCAACAACCTTGGAACCTGTAAGTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCGGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAAGTGTGCAAGATA
 GAGCATGTACACATGATAGGTGAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGTGGGAGACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCCAGGAAT
 GATGAGGTATGAAGACTACCAAAATCATATTGGGTGTTTTGTGGCCATCACACTCATGGCTGAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGACCATTGCGGAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGGCCACTGCCATGCTGCTATGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAGCTTAACACAATAAATCAATACA
 CAGTTCAGTGCATGAACGTTATTGATCCGAATGAACCTTAAGACAATGTACAGAGACTCAAACTTAAACA
 TTTACAGAGTTACAAAAAACAAACATCAAAAAAAGACAGTATTATAAAAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNLTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
YISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKLELDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSITSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTQDTGMYTCMVNSVGN
TTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTDNNVGTPVVDWETTNVTTSLTPQ
STRSTKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGCGCGGGGCCGGCTCCCGCCGGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCCAGGGCGCCGCGCCAGCTCGCCCGAGGTCGGTCGGA
 GCGCGCCGGCGCCCGGAGGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCCTCCTCTTCTCCTCTTGCTAGTTTCTACTATTTTGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGCACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGGAACCAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCGATTTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAACTAGGATT
 GACTACAACCCCTGGACGAGTTCTGCTGCAGAACTTACCATGTCTACTCTGGACTGTA
 CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAACGTACAGT
 ATGTACAAGACTCCGCACTGGTTGCAGGAGCAGTGACAGGCATAGTGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAACCCAGCT
 CCTCTTCTCAGGCTCTGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAA
 AGTGCCCTCACGAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGCT**TGA**ATTACAATTGACTTTGACTCCACGCTTCTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTATTGGAGCTCAAGTCACCAAGCCACACAACAGATGAGAGGTCTCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTGAGTATGAGCATTCTTCTTATACAATACCAACAAAGCAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AAGTGAAATATACCTAAACTTTTAAATGTGGGATATTTGTATCAGTGCTTTGATTACAAAT
 TTTCAAGAGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTTATTGGATT
 ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGCTACACCATGTAC
 TGAGCTAACCACCTTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTGCATAAGGTTGGATATTAATTTCAAGGGGAGTTGAAATAGTTGGGAGATGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAAGGAGACAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAT
 CAGATGCCCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCAAT
 TATCAAGCTCCTTAGAAAGAAATTTCTTAGAGAAAAGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAACACGAATTGCAAGACTGG
 GTGGACTAGAAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTTAGGAAAATCCAGAGGTGGAGGTGCGATGAGCGCAGATTATGCG
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCCGCGCCACGGCAGCGCAGCA
 CCATGCGCCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGGATATCACTACT
 CCTGAAGAGATGATTGAAAAGCCAAAGGGGAACTGCCATTCTGCCATGCAAAATTACGCTTAGTCCCGAAGA
 CCGAGGACCCCTGGACATCGAGTGGCTGATATCAACAGCTGATAATCAGAAGTGGATCAGTGATTTATTTAT
 ATTCTGGAGACAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTACAGTAAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTAAACGAATTTCAACTGTGAGATATTGGCAGATATCAGTGCAAAAGTGA
 AAAAGCTCCTGGTGTGCAAAATGAAGAGATTCACTGGTAGTCTCTGTTAAAGCCTTCAGGTGCGAGATTGTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG
 TATGAGTGGCAAAATTTGTCTGACTCAGACAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTGTATC
 AGTGCTCTGTTGCGTCTAAACGTTGTCCCTCCTTCAAAATGAAGTGGAGTAAATGACAGGAGCCATTATAGGAAT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGCGTAAAAAGCGCAGAGAAGAAAAATATGAAAA
 GGAAGTTTCATCAGGATATCAGGGAAGATGTGCCACCTCCAAAGAGCGGTACGTCCTGCGCAGAAAGTACATCG
 GCAGTAATCATTTCATCCCTGGGGTCCATGTCTCCTTCCAAACATGGAAGGATATTCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAAGCCACTCTCAGAGTCCGACTCTCCCACTGCTAAGTTCAAGTACCCCTTACAA
 GACTGATGGAAATACAGTTGTATTAATAATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCTGTCAAAATTAGTACGAGCCAAATCTTTGT
 TAAAAAACCCCTATGTATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCACTAACAA
 ATTTTTAACTTTTCATATGATATCTGATATGTGGTCTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTACGTTCTGTTTAAATGTTTTGCTATTAGTTAAATACATTGAAGGGAATACCCG
 TTCTTTTCCCTTTTATGCACACACAGAAACACGCGTTGTCTAGTCCCTCAAACTATTTTTTATTGTCAACTACA
 TGATTTACACATACTCTTTAAACACACGACATAAAATAGATTTCCTGTATATAAATAACTTACATACGCTCCA
 TAAAGTAAATTTCAAAAGGTGCTAGAACAAATCGTCCACTTCTCAGTGTCTCTGATATCCACAGAGTTGATGG
 ACAATATATAAATACTCAGTCCATATTAATAACTTAGGCACCTTGACTAACTTTAATAAAATTTCTCAAACTA
 TATCAATATTTCAAGTGATATATTTTTTAAGAAAGATTATCTCAATAACTTCTATAAAATTAAGTTTGATGG
 TTTGGCCCTCTAACTTCACTACATATTAGTAAGAAGTTTAACTTTAATGTGTAGTAAAGTTTATTTACCTT
 TTTCTCAACATGACACCAACACATCAAAACGAAGTTAGTGAGTGCTAACATGTGAGGATTAACTCAGTGAAT
 TCCGCTCACAATGCATTTCCAGGAGGAGTACCCTATGTCAGTGGAAATGGCGATATGGTTTATTTTCTCCCT
 TGATTTGGATAACCAATGGAACAGGAGGAGTATGATTTCTGATGCCATTCCCTCGATACATTCCTGGCTT
 TTTTCTGGGCAAGGTTGCCATTTGGAAGAGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGACACAT
 TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACACACT
 GAGATCACATCTAAGTGACACTCCTATTGTAGGTTCAAAATACATTAAAACTCATGTGTAATAGGCGTATAA
 TGTTATACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAACTCAACACAGTACTTCTAAACCAA
 CTTCACCAAAAAAGCCAAACATGGAACGAATGGAAGCTTGTAGGACATGCTGTGTTTAGTCCAGTGGTTT
 CACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAATCAATTTGGAGCTGGAGGCCATTTATCTT
 AGCAACTAATGTGCAAGAACAGAAATCACTACCGCATGTTCTCATCTAAGTGGGAGGTAAATGATAAGAACT
 TATGAACCTAAAGAGGAAACAAATAGACATTTGGATCTATTTGAGAGGGGAGGTTGGGAGAGGAAAGGAGCA
 GAAAGATAACTATTGAGTACTGCTTTACACTGGGTGATGAAATAATATGTACACAAATCTCGCTGTGACACA
 TGTTTACCTATGGAACAACTTTCATGTGATCCCTAAACCTAAAAATAAAGTTTAAAAAAGGAAAAAAGGAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLLCFVLLCGVVDFAFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMP
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRRKKREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSILGSMSPSNM
EGYSKTQYNQVPSEDFERTFPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTCAGCATCACTTACAGGACCAGAGGGACAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCGAAAATTCACAAAGC
 TCTGAATGCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTTCA
 AACAGTCTCCCTTCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACCTCTATT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAAATCCTTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGACATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCAGCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARFFCPPLLATASQMVMVLPCLGFTLLLSQVSGAQGEFHFPGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTLILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCAGGTCCAACCTGCACCTC
 GGTTCATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTCGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCCTGGTCACTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCCGATGACCCCGGCCCGGCCCTCCTGTTCACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTGC
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGACGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGTGTAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCTAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCC
 GTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
 GGTCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCCTCTGCCGAGACCCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACCCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGCTCTCATAGAGCTGGGTACGAGTGGGCAAAACAACCTTC
 CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCCCTCGAAGCCGCCCTCAAGAACTTCACCC
 CTTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCT
 CTTCTCTGTCTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGAACTCCACGCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCGTATGCCAAAAGAGGTTGTGCCCTAGCCTG
 GGCCCCACCCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCAACCACAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTCACTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCTACTGTGTGCTTCCATCCTGCA
 TTAAAATTCAGTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAAGSPEGAGM
 TTVQTTITGSDPEEAIFDTLCTDDSSSEAKLTMDILTTLAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVE
 TSPSYVKVSGAAPVSIAGSAVGKTTSFAGSSASSYSPEAALKNFPTSETPTMDIATKGP
 FPTSRLPLPSVPPTTTNSSRGNTSLAKITTSAKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTCGCCGCTCTCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAAATTTGCTTCTCGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAATTTTCAACAAGCAGTCACCTCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTTGATCTCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCACGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCATTCTC
 AGCCTCCACAGACCTCATTTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACCTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAAATGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCTCTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACACTAAAGGATGGAACCTCGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAATGAATGAGTTTCTGCTGACTTGTGATGCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCCGAACCTCCGTCTC
 CTGGGTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATGCACCTCTCGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAAATTAGTAATTTTGGGTAATCTGTCTCAAAATTTAGCTAAGAAACCAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCAGATAAATCAAC
 TGTTTATATCAATTTCTAATGAGATTGCTTTTCTTTTATATGGATTCTTTAAACCTAAT
 CCAGATGTAGTTTCTTCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTRLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPCYLFCCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSEQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTINTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFKEKWLIGSLLFGVLFLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCTCAGCGCCAGAA**ATG**CGGCTTCTGGTCTGCTATGGGGTGGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTCTTGGCACCATCTATGCAGAAAGAAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCTGCTGTCTCCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCACAGCAGCTCTCTCTCTGCAGGGAGCTCCCGCCCCCATGCGAG
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGTCTCAGCAGTGGCAGCTCTAAGCCCAAG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGAGCCTTCTGTACG
 CGCAGGGCTGATCGCCTTCTGCAGCCACCTGCTCTGTGGAGAAAGGAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTCGCGAGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCCGATTCCTCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGGCTCTCCCCACCCTCCCAAGGCTCTCTCTTGATGTTCCA
 GCCTGACCTAGAAAGGTTTGTCTCAGCCCTGGAGCCAGGCGGTGGCCCTTGCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTGATGCCAGTGTGCGGACCCTGCCTTCCCTCCCACTCCAGACCCCACTTGTCTTCCCTCC
 TGGCGTCTCAGACTTAGTCCCAAGGCTCTCTGCTATCAGCTGGTGTGTAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCTAACAATGCCCAAGTACTGTGCGACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCTTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTGACATTTGCAGGATAAGCCAGGACCGGCACAGAAAGTGG
 TTGCCCTTTCACCTTGGCCCTCCCTGNCCTATGCTTCTTGGCTTTGGAAAAATGATGAAGA
 AAACCTTTGGCTCCTTCTTGTCTGGAAGAGGTTACTTGGCTATGGGTCTGGTGGCTAGAGA
 GAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGTGGTGAAGTA
 GCACAACCTACTATTTTTTTTCTTTTCCATTTATTTGTTTTTGAAGACAGAATCTCGTGTCT
 GTGCGCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCTCCTGGGTTCAAGTGATT
 CTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGCTTGAACCTCTGAC
 CTCAAATGAGCCTCTGCTCTCAGTCTCCCAAAATGGCGGATTACAGGATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTGAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCACCATAGTCTCACACAGACATCAT
 TATTTCTGTTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTCT
 TTTACAGAGCAATTATCTTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTTCCAGCACTTCTGTGTTTTACAGACCTTTTATAAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTLDAGEYWC GVEKRGPDESLLISLFV
FPGPCCPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG
TSQYGHERTSQYTGTSPHPATSPFPAGSSRPMPQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128